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Sequence:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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   Issued_Patents_NA: *
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Listing first 90 summaries
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Copyright (c) 1993 - 2002
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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   153338381 residues
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US-09-225-575-123
US-09-020-956-20
US-09-030-607-20
US-09-439-313-20
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US-09-171-209-38
                                                                                                                                                                                    US-08-248-474-36

US-08-756-849-36

US-08-716-942-20

US-09-130-337A-20

5196523-1

US-08-804-372A-23

US-09-404-879A-372

5196523-2

5196523-2
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Sequence 20, Appl Patent No. 5196523 Sequence 372, Appl Sequence 15, Appl Sequence 15, Appl Sequence 123, Appl Sequence 20, Appl Sequence 21, Appl Sequence 25, Appl Sequence 55, Appl Sequence 55, Appl Sequence 27, Appl Sequence 1, Appl Sequence 1, Appl Sequence 27, Appl Sequence 1, Appl Sequence 27, Appl Sequence 1, Appl Sequence 27, Appl Sequence 1, Appli Sequence 1, Appli Sequence 31, Appli
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ALIGNMENTS

NESULT 1 VUS-08-248-474-36 VUS-08-248-474-36 V3: Sequence 36, Application US/08248474 Patent No. 5612471 ; GENERAL INFORMATION:

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RESULT 2
US-08-756-849-36
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                                                                                                                                                                                                                                                                                            Sequence 36, Applic
Patent No. 6093810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                         APPLICANT: Bird, David Mck
APPLICANT: Wilson, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 23
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: NEWATODE-INDUCE GENES IN TOMATO
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                STREET: Two Embarcac
CITY: San Francisco
                                                                                                                                    ADDRESSEE: Townsend and townsend Eighth Floor
                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1..272
OTHER INFORMATION: /standard_name= "DB# 155"
SOFTWARE:
                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                 97 CCAATATTATTTACCACG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 25-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bastian, Kevin L
                                                                                                                     California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             California
                                                                                                                                                                                                                                                                                                            Application US/08756849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                           Bird, David McK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McK. BIRD, David
                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                      Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum cv 'Rutgers Large
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52.6%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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3.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5849491
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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     PRIOR APPLICATION UNMBER 60/004,157
APPLICATION NUMBER 60/004,157
FILING DATE: 20-Sep-95
ATTORNEY/AGENT INFORMATION:
                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 25-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                             CLASSIFICATION: 435
                                                                                               FILING DATE:
                                                                                                                                                                                                                                     ZIP:
                                                                                                                                                                                                                                                                      STREET: 1992 CTTY: Yorktown Heights
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: 1..272
OTHER_INFORMATION: /standard_name= "DB# 155"
                                                                                                                APPLICATION NUMBER:
                                                                                                                                                SOFTWARE: Word Perfect
                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                    COMPUTER:
                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 CCAATATTATTTTACCACG 115
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TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/756,849 FILING DATE: 26-NOV-1996
                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08716942
                                                                                                                                                                                                                                                                                                   E: Oppedahl & Larson
1992 Commerce Street, Suite 309
                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                            Yap, Wai Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Warren, R. Antony J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Radomski, Christopher C. A. Seow, Kah Tong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Terragen Diversity Inc
                                                                                                                                                                               IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                        METHOD FOR ISOLATING XYLANASE GENE SEQUENCES FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD COMPOSITIONS OBTAINED THEREBY
                                                                                                                                                                  DOS 5.0
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52.6%;
                                                                                                                US/08/716,942
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Pred. No. 3.6e+02;
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RESULT 5
5196523-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 4
US-09-130-337A-20/c
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                                                                                                                                                                                                                                                   US-09-130-337A-20
             Patent No. 5196523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/09130337A Patent No. 6441148
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                                                                                                                                                                                            Query Match
Best Local
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                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/130,337A CURRENT FILING DATE: 1998-08-06 PRIOR APPLICATION NUMBER: 08/716,942 PRIOR FILING DATE: 1996-09-20 PRIOR APPLICATION NUMBER: 60/004,157 PRIOR FILING DATE: 1995-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Warren, RAJ
APPLICANT: Yap, WH
TITLE OF INVENTION: METHOD FOR AMPLIFICATION OF XYLANASE GENE FRAGMENTS
TITLE OF INVENTION: FROM SOIL DNA, COMPOSITIONS USEFUL IN SUCH METHOD AND COMPOSITIC
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 9993-004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Radomski, CCA
                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown organism
                                                                                                                                                                                                                                                                  \begin{tabular}{ll} \textbf{FEATURE:}\\ \textbf{OTHER INFORMATION:} & \textbf{Description of unknown organism:} \\ \end{tabular}
                                                                                                                                                                                                                                                                                                                                        LENGTH: 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: TE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 245-3252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE: no FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: ge
APPLICANT: LEE, AMY S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 CCAATGGTTGTGGCCCACG 199
                                                                                                     217 CCAATGGTTGTGGCCCACG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (914) 962-4330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CCAATNNNNNNNNCCACG 19
                                                                                                                                         1 CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment of xylanase gene from degenerate primer amplification of soil {\tt DNA}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic DNA
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                                                                                                                                                                                            52.6%;
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52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                  Score 10; DB 4; pred. No. 3.7e+02; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 10; DB 2;
Pred. No. 3.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 296;
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                                                                                                                                                                                                             Length 296;
                                                                                                                                                                                                                                                                      soil microbe
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RESULT 6
US-08-804-372A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; SEQ ID NO:1:
                                                                 US-08-804-372A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/08804372A Patent No. 6183753
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Best Local Similarity
               Query Match
Best Local Similarity
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APPLICANT: Cochra
                                                                                                                                                                                                                TELEFAX: (212) 391-052 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-MAY-1989
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wild, Martha A. APPLICANT: Winslow, Barbara J. TITLE OF INVENTION: Recombinan TITLE OF INVENTION: Thereof
                                                                              MOLECULE
HYPOTHETICAL: N
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
                                                                                                                                                                                                                                               TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 CCAATCGGAGGCCTCCACG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 282,880 FILING DATE: 05-DEC-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 01-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 690,951
                                                                                                                                                                                                                                                                                NAME: White, John P.
REGISTRATION NUMBER: 28
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/804,372A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: New York
STATE: New Yor
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                                                                                                                                TOPOLOGY:
                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10036
                                                                                                                                                             nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
 Conservative
                                                                                                                                                                                                                                   (212) 391-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cochran, Mark D.
                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                linear
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                                                                                                  NO
                                                                                                               DNA (genomic)
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52.6%;
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52.6%;
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Pred. No. 3.8e+02;
                   Score 10; DB 4;
Pred. No. 3.9e+02
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                                  DB 4;
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                                Length 387;
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Gaps
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Matches

10;

0; Mismatches

Indels

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1 CCAATNUNNNNNNCCACG 19

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5196533-22
;PAINT NO. 5196523
;PAINT NO. 5196523
;PAINT NO. 5196523
;TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
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                                                                                                                                                                     RESULT 9
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US-09-404-899A-372/c
Sequence 372, Application US/09404879A
Patent No. 6468846
GENERAL INFORMATION:
                               CALCIUM AND TEMPERATURE
NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : APPLICANT: LEE, AMY S.
TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE, CALCIUM AND TEMPERATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 01-JAN-1985 SEQ ID NO:23:
                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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Best Local :
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APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 282,880
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 690,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 28 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 392
                                                                                                                                                                                                                      311 CCAATCGGAGGCCTCCACG 329
FILING DATE: 19-MAY-1989
                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 CCAATCAAAAGCTGCCACG 280
                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 399
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FILING DATE: 19-MAY-1989
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52.6%;
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               US/07/354,988
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Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                             Length 399;
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                                                                                                                                                                                                                                                                                            Indels
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XRESULT 10
US-08-609-657-15
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US-08-609-657-15
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                                                                                                                                                   Matches
                                                                                                                                                                                                               Query Match
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (716) 849-0349 INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS/ Microsoft Windows 3.1
SOPTWARE: Wordperfect for Windows 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (716) 856-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 01 March 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 282,880
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 690,951
FILING DATE: 01-JAN-1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stoler, Daniel L. TITLE OF INVENTION: Mammalia TITLE OF INVENTION: Element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 10
361 CCAATTGTATGTAACCACG 379
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                                                                                                                                           Local Similarity hes 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Nelson, M. Bud
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/609,657 FILING DATE: 01 March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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                                                                       1 CCAATUNNUNUNUCCACG 19
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                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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52.6%;
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52.6%; Pred. No. 3.9e+02;
Nismatches 9;
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                                                                                                                                Score 10; DB 1; Le
Pred. No. 3.9e+02;
0; Mismatches 9;
                                                                                                                                                                                                            Length 424;
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RESULT 11 US-09-257-584-8/c ; Sequence 8, Application US/09257584A

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US-09-257-584-8
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US-09-222-575-123
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TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 5718-33, 035718/175218
CURRENT APPLICATION NUMBER: US/09/257,584A
CURRENT FILING DATE: 1999-02-25
EARLIER REPLICATION NUMBER: 60/076,075
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 123, Application US/09222575 Patent No. 6387697
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer TITLE OF INVENTION: and Methods for Their Use FILE REFERENCE: 210121.470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Dav
                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/222,575
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
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ORGANISM: Zea mays
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                                                                                                                                                                                                                                  NAME/KEY: modified_base
LOCATION: (152)
OTHER INFORMATION: Where n is
NAME/KEY: modified_base
LOCATION: (373)
                                                                                                                                                                                                                 LOCATION: (373)
OTHER INFORMATION: Where
                                                                                                                                                                                                                                                                                                                                             ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
                 NAME/KEY: modified_base LOCATION: (502)
                                                     OTHER INFORMATION: Where n is
                                                                      NAME/KEY: modified_base LOCATION: (496)
                                                                                                        OTHER INFORMATION: Where
                                                                                                                                           NAME/KEY: modified_base
                                                                                                                                                              OTHER INFORMATION: Where
                                                                                                                                                                                 LOCATION:
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OTHER INFORMATION: Where n is a, c,
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Mitcham, Jennifer L.
                                                                                                                             (494)
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52.6%;
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Pred. No.
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; Patent No. 6261562
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Best Local Similarity 52.6%;
Matches 10; Conservative
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                                                                                                                                                          Sequence 20, Application US/09030607 Patent No. 6262245
                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: XU., Jiangchun APPLICANT: Dilin, Davin C. APPLICANT: Dilin, Davin C. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Maki, David J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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                                                                 APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUN NUMBER OF SEQUENCES: 224
                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
                                                   CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                        303 CCAATTGTTTTNGCCACG 321
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                 STREET:
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Seattle
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                                    SEED and BERRY LLP
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                                                                                        COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
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Pred. No. 4.1e+02;
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Pred. No. 4.3e+02;
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RESULT 15
US-09-605-785-20
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                                                                                 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 20 LENGTH: 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 20, Application US/09605785 Patent No. 6321716
                                                                                                                                                                      APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 20121.427C16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                             CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Xu, Jiangchun
LOCATION: (1)...(754)
              NAME/KEY: misc_feature
                                   FEATURE:
                                                 ORGANISM: Homo sapien
                                                                   TYPE: DNA
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 754 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
FILING DATE: 25-FEE
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                   Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                   Stolk,
                                                                                                                                                                                                                                                                                                                 Vedvick, Thomas S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harlocker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                 Fanger, Gary R
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57.9%; Pred. No. 4.3e+02;
^. Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Susan L.
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APPLICANT: SOIK, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 754
TYPE: DNA
ORGANISM: Homo sapien
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US-09-352-616A-20
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SOFTWARE: Fa
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Patent No. 6395278
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
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                                                                                 APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
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APPLICANT:
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                                         CURRENT APPLICATION NUMBER: US/09/352,616A
CURRENT FILING DATE: 1999-07-13
CURRENT OF SEQ ID NOS: 472
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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                           FastSEQ for Windows Version 3.0
                                                                                                                                                                            Jiang, Yuqui
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57.9%;
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Pred. No. 4.3e+02;
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US-09-232-149A-20
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; OTHER INFORMATION: n = A,T,C or G
US-09-352-616A-20
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; LOCATION: (1)...(754)
; OTHER INFORMATION: n = A,T,C or G
US-09-232-149A-20
                                                                                                                                                                                                                                                                                                                                                                                       RESULT 19
US-09-171-209-38
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CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 20
LENGTH: 754
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapien
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ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Needle & Rosenberg, P.C.
STREET: 127 Peachtree Street, Suite 1200
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 83
                                                                                                                                                                                                                                                       TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
                                                                                                                                                                                                                                                                                                               APPLICANT: VANDERBILT UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11;
                                                                                  COUNTRY: USĂ
ZIP: 30303-1811
                                                                                                                    CITY: Atlanta
STATE: Georgia
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57.9%;
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Pred. No. 4.3e+02;
""" matches 8;
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Pred. No. 4.3e+02;
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                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: CH 0016/97
FILING DATE: 31 DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meisg. J. Timothy
REGISTRATION NUMBER: 38,241
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 38: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/998,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Philippsen, APPLICANT: Pohlmann, R
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
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REFERENCE/DOCKET NUMBER: PF
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                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 Match 52.6%; Score 10; DB 4; Length 843; Local Similarity 52.6%; Pred. No. 4.4e+02; nes 10; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U
                                                                                                                                                                                               FILING DATE:
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APPLICATION NUMBER: US/09/171,209
FILING DATE: 08-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 404 688 0770
TELEFAX: 404 688 9880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Selby, Elizabeth REGISTRATION NUMBER: 38,298 REFERENCE/DOCKET NUMBER: 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/US97/06067 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08998416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wendland, Jurgen
Knechtle, Philipp
Rebischung, Corinne
REPUISCHUNG, CORINNE
WENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pohlmann, Rainer
Steiner, Sabine
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                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No. 6239264artis Corporation
                                                                                                                                                                                          24-DEC-1997
                         PF/5-30306/A/CGC1976
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US-09-541-941B-21/c
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APPLICANT: Wang, Jun
APPLICANT: Shaw, Panc
APPLICANT: Paul, Pui
APPLICANT: Ngan, But,
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENCTH: 904
                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09137855B Patent No. 6242237
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                    APPLICANT: Kofod, Lene V.
APPLICANT: Kauppinen, Markus S.
APPLICANT: Andersen, Lene N.
APPLICANT: Clausen, Ib G.
APPLICANT: Mullertz, Anette
TITLE OF INVENTION: An Enzyme With Galactanase Activity
FILE REFERENCE: 4686.204-US
EARLIER APPLICATION NUMBER: 0233/96
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: 0235/96
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
EARLIER APPLICATION NUMBER: PCT/DK97/00092
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                                                                                                                        CURRENT APPLICATION NUMBER: US/09/137,855B
CURRENT FILING DATE: 1998-08-21
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Paul, Pui-Hay
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
TITLE OF INVENTION: POLYMERASE CHAIN REACTION - RESTRICTION FRAGMENT LENGTH POLYMORPH
TITLE OF INVENTION: FOR THE AUTHENTICATION OF HERBAL CHINESE MEDICINES
TILE REFERENCE: 2913/52188-ZA
CURRENT APPLICATION NUMBER: US/09/541,941B
CURRENT FILING DATE: 2000-04-03
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TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
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ORGANISM: Campanumoea Javanica Blume
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.6%;
Local Similarity 52.6%;
es 10; Conservation
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STRANDEDNESS: single
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; TYPE: DNA ; ORGANISM: Myceliophthora thermophila US-09-137-855-1
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LENGTH: 1117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rafalski, J. Antoni
APPLICANT: Falco, S. Carl
TITLE OF INVENTION: Ornithine Biosynthesis Enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/093,209
EARLIER FILING DATE: July 17, 1998
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/347,819
CURRENT FILING DATE: 1999-07-02
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NAME/KEY: unsure LOCATION: (1100)
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                                                         NAME/KEY:
                                                                            FEATURE:
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(1043)
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(320)
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(229)
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Best Local S
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OTHER INFORMATION: n = a, US-09-541-941B-27
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
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PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                      APPLICANT: Wang, Jun
APPLICANT: Shaw, Pang Chui
APPLICANT: Shaw, Pang Chui
APPLICANT: Paul, Pui-Hay
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
APPLICANT: Ngan, But/and Fai Ngor Karenda Ngan
TITLE OF INVENTION: FOR THE AUTHENTICATION OF HERBAL CHINESE MEDICINES
FILE REFERENCE: 2913/52188-ZA
CURRENT APPLICATION NUMBER: US/09/541,941B
CURRENT FILING DATE: 2000-04-03
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                                                                                                                                                                  SEQ ID NO 27
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                                                                                                                                                                                 SOFTWARE: PatentIn version 3.1
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                                         FEATURE:
NAME/KEY: misc_feature
LOCATION: (100)..(100)
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                                                                                                     TYPE: DNA ORGANISM: Pheretima Aspergillus
                                                                                                                                            LENGTH:
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52.6%;
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Pred. No. 4.6e+02;
Pred. No. 4.76e+02; Indels
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                            g, or u
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                                                                            TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEFAX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5871910man F.
REGISTRATION NUMBER: 24,618
REFERENCE/POCKET NUMBER: 660-060
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                         FILING DATE: 29-OCT-PRIOR APPLICATION DATA:
                                MOLECULE TYPE:
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                  FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/OFILING DATE: 05-AUG-1994
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                                                                                                                                                                                                                                                                                        FILING DATE: 31 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/FR/91/00855
FILING DATE: 29-OCT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                    TOPOLOGY:
                                                                   STRANDEDNESS: unknown
NAME/KEY: CDS
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SYSTEM: PC-DOS/MS-DOS
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                                                    unknown
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                                      DNA (genomic)
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52.6%;
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 Mismatches

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Pred. No. 4.7e+02;
                                                                                                                                                                                                                              660-060-0 PCT
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LOCATION:

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US-08-286-819A-31
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                                                                                               INFORMATION FOR SEQ ID NO:
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     MOLECULE TYPE:
                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5871910man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            FILING DATE: 29-OCT-1991
PRIOR APPLICATION DATA:
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APPLICANT: COURVALIN, PARRICE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: POLYPEPTIDES IMPLICATED IN THE
TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOF
TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/174,682
FILING DATE: 28-DEC-1993
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                  STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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ADDRESSEE:
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                                       nucleic acid
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                                                                                                           : (703) 413-2220
248855 OPAT UR
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                                                                                                                                               (703) 413-3000
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DNA (genomic)
                                                                                                                                                                                                                                                           31-OCT-1990
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                               unknown
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                                                                                                                                                                             660-060-0 PCT
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Pred. No. 4.8e+02;
0; Mismatches 9
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RESULT 28
US-08-980-357-7
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                                                                                                                        TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
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                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
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                   FEATURE:
                                 MOLECULE TYPE:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICATION NUMBER:
FILING DATE: 10-AUG-
PRIOR APPLICATION DATA:
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PRICE APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SCIFTWARE: PatentIn Release #1.0, Version #1.25
CURFERT APPLICATION DATA:
AFPLICATION NUMBER: US/08/980,357
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MEDIUM TYPE: Floppy disk
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NAME/KEY: CDS
                                                 TOPOLOGY:
                                                             STRANDEDNESS:
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                                                                                                                                                                                                                  NAME: Oblon, No. 60 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: FR 90 FILING DATE: 31-0CT-1990
                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/
FILING DATE: 29-OCT-1991
                                                                                            LENGTH:
                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-AUGAPPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US OF FILING DATE: 05-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Arlington
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                                                                          nucleic acid
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Y: U.S.A.
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1755 S. Jefferson Davis Highway, Suite 400
                                              unknown
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MOLINAS, CATHERINE
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                            DNA (genomic)
                                                           unknown
                                                                                                                                                                                                                                                                                                                                                          UMBER: US 07/917,146
10-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                        JMBER: US 08/174,682
28-DEC-1993
                                                                                                                                                      413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.6%;
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                                                                                                                                                                                                 660-060-0 PCT
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Pred. No. 4.8e+02;
"""matches 9;
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; MOLECULE TYPE: DNA (genomic) US-08-980-357-31
                                               TELEFAX: (703) 413-3000;
TELEFAX: (703) 413-2220;
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 1347 base pairs
TYPE: nucleic acid
STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: COURVALIN, PATRICE TITLE OF INVENTION: PATRICE BACTERIA, NUCLEOTIDES, IN PARTICULAR TITLE OF INVENTION: EXPRESSION OF RESISTANCE TO GLYCOPEPTIDES, IN PARTICULAR TITLE OF INVENTION: IN GRAM-POSITIVE BACTERIA, NUCLEOTIDE SEQUENCE CODING FOR TITLE OF INVENTION: THESE POLYPEPTIDES AND USE FOR DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                         FILING DATE: 31-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US U8/200, CAPPLICATION NUMBER: US 08/174,682
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FR 90
FILTING DATE: 31-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/917,146 FILING DATE: 10-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US OF FILING DATE: 28-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/FR/91/00855 FILING DATE: 29-OCT-1991
                                         TOPOLOGY:
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1755 S. Jefferson Davis Highway, Suite 400
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pred. No. 4.8e+02;
pred. No. 4.8e+02; Indels
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; Sequence 1389, Application US/09134001C ; Patent No. 6380370
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                                                                             Вb
                  Search completed: November 16, 2002, 03:33:38
                                                                                                                                                                                                                                                                      ; SEQ ID NO 1389
; LENGTH: 1377
; TYPE: DNA
Job time : 50 secs
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Best Local Similarity 52.6%;
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PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: GTC-007
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Score Match Query $\ldots$ Length DB $\begin{smallmatrix} \mathsf{O} & \mathsf{O}$ DO412LMS2 AX310584 AF229112S3 AX386623 AX033507 AF305966 AX033504 AX033505 HUMETG05 AX072778 AX033508 E44205 AF271990 AX343728 AX033516 AX033517 HUMCG3A02 AF479941 AX343726 AX443752 AX447733 E44206 E44207 E44208 E44210 E44211 E44211 E44212 E44213 E28807 E28808 E28809 E28804 E28805 E28806 E28802 E28803 AY020507 G31118 HS8C1R DY421FOS2 AF229139 CNS01951 ID AF229137 DY426FOS2 AF229143 BTU10392 AX313758 AX439681 AX156202 RTU74410 AY020067 AX209173 E44202 AF386187 AX302886 E28800 E44234 AF229147 AF229145 E44214 Endoplasmic AX443752 Sequence AX447733 Sequence E44234 Endoplasmic AF305966 Haemonchu AY029608 Mesocrice AF163413 Downingia AX310584 Sequence AF229114 Downingia AX316503 Sequence AX39681 Sequence AX39681 Sequence AX156202 Sequence AX156202 Sequence AX156201 Sequence AX033517 Sequence AX033504 Sequence AX033505 Sequence D10343 Homo Sapien AX072778 Sequence AX033508 Sequence AX033507 Sequence AF271990 Human ade AX343728 Sequence AX033516 Sequence AX033517 Sequence AY020067 Oryza sat AX209173 Sequence AY020507 Oryza sat G31118 human STS: Z66326 H.sapiens C AF386187 Homo sapi E44202 E44206 E44207 E44209 E44209 E44210 E44211 E44211 E44211 E44213 E28807 E28808 E28809 E28805 E28806 E28797 E28801 AF163422 AF229139 AL111214 AF229137 AF229137 AF229143 AF229143 AF229143 M10797 Human alpha AF479941 Saccharon AX343726 Sequence E28802 Description U10392 Bos taurus AX313758 Sequence AF229145 Downingia E28800 Endoplasmic E44205 Endoplasmic AX302886 B Endoplasmic Endoplasmic Endoplasmic Endoplasmic Endoplasmic Endoplasmic Endoplasmic Endoplasmic Human alpha 11 Saccharom Endoplasmic Sequence Downingia Downingia Downingia Downingia Downingia Oryza sat Sequence Botrytis Downingia Downingia

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      unidentified. unidentified
                      E28797.1 GI:13020851 JP 1999243959-A/1.
                                    E28797 19 bp DNA linear PAT 1 Endoplasmic reticulum stress-response regulatory element.
unclassified
                                                                                                                          19;
                                                                                                                                                                                                         Patent: WO 0171018-A 1 27-SEP-2001;
THE BOARD OF TRUSTEES OF THE UNIVERSITY OF ARKANSAS (US)
                                                                                                                                                                                                                               Secreting products from skin by adeno-associated virus (aav) gene
                                                                                                                                                                                                                           transfer
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                                                                                                                                                                                                                                                          unclassified
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100.0%;
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Z61059 H.sapiens C
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   1 Similarity
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                                                                                                                              HSP
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                                                                                                                                                                                                                                                                                                              Hideo, Y., Hideki, Y. and Takashi, Y.
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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E28801
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Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element Patent: JP 199943959-A 1 14-SEP-1999;
HSP RESEARCH INST INC
OS Unidentified
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   Conservative
                                                                                                                          enhancer
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
                                                                                                                                                             Strandedness: Double;
                                                                                                                                                   Topology: Linear;
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                                                                                                                                                                                                                                       Homo sapiens (human)
JP 199243959-A/5
14-SEP-1999
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
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14-SEP-1999
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                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
9 c 5 g
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RL Patent: JP 199243959-A 6 14-SEP-1999;
HSP RESEARCH INST INC
OS Mus SP. (mouse)
PN JP 199243959-A/6
PD 14-SEP-1999
PN JP 199243959-A/6
PD 14-SEP-1999
PN JP 1998052453
PF HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
PC C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00,C12N1
PC A61K37/02
CC Strandedness: Double;
FH Key
FH Key
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Hideo,Y., Hideki,Y. and Takashi,Y.
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Endoplasmic reticulum stress-response regulatory element
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                       Rattus sp.
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HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
A61K37/02
                                                                                                    Rattus sp. (rat)
JP 1999243959-A/7
                                                                    04-MAR-1998 JP 1998052453
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RESULT 6
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Gallus sp. Gallus sp.
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                                                         Endoplasmic reticulum stress-response regulatory element
                        JP 1999243959-A/9.
                                                                       E28805
                                   E28805.1
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Homo sapiens (human)
JP 1999243959-A/8
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C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
A61K37/02
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                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                 Strandedness: Double;
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/db_xref="taxon:10118"
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                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.8e+04;

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Pred. No. 1.8e+04;
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E28806
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C12N15/09,A61K35/74,A61K35/76,A61K38/00,A61K48/00,C12N15/00,
                                                                                                                                                                                                                                                                                                            Topology: Linear;
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
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/db_xref="taxon:9606"
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/db_xref="taxon:9036"
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Hideo, Y., Hideki, Y. and Takashi, Y. Endoplasmic reticulum stress-response regulatory element Patent: JP 1999243959-A 12 14-SEP-1999;
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JP 1999243959-A/12.
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04-MAR-1998 JP 1998052453
                            Homo sapiens (human)
JP 1999243959-A/12
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A61K37/02
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JP 1999243959-A/11
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                                                                                                    CCAATGAGGGTCGACCACG 19
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                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
Hidee, Y., Hideki, Y. and Takashi, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E28809
E28809.1 GI:13020863
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Endoplasmic reticulum stress transcription factor. E44202
E44202.1 GI:18633455
                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Endoplasmic reticulum stress-response regulatory element
Patent: JP 1999243959-A 13 14-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endoplasmic reticulum stress-response regulatory element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JP 1999243959-A/13.
                                      E44202
                                                                                                                                                                Similarity
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Mus sp. (mouse)
JP 1999243959-A/13
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C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
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                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                   Strandedness: Double;
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                                                                                                                                                                                                                                                                                                                                          HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/00,
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04-MAR-1998 JP 1998052453
                                                                                                                                                                                                                                                                                                      Popology: Linear;
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/db_xref="taxon:9606"
6 c 5 g
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6 c 6 g
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                                                                                                                                                                52.6%;
52.6%;
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Pred. No. 1.8e+04
                                                                                                                                                                Score 10;
Pred. No.
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OS
PN
PD
PF
                                                                                     TAKASHI YURA
PC C12N15/00, PC
(C12N15/00, PC
CC
FH Key
FT Source
FT
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CC CC Location/Qualifiers
FT source 1 19
FT fource /organism='Artificial Sequence'.
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                                                                                                                                                                                                                                                                                 Endoplasmic reticulum stress transcription factor
Patent: JP 2001054391-A 5 27-FEB-2001;
HSP RESEARCH INST INC
                                                                                                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoplasmic reticulum stress transcription factor Patent: JP 2001054391-A 1 27-FEB-2001;
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1 (bases 1 to 19)
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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11-NOV-1999 JP 1999321743
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JP 2001054391-A/5
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5 c 1 g
          /organism="Homo sapiens"
/db_xref="taxon:9606"
9 c 5 g
                                                                    /organism='Homo sapiens (human)'
Location/Qualifiers
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VERSION
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E44207
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                                                AUTHORS
TITLE
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TITLE
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                                 JOURNAL
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Patent: JP 2001054391-A 6 27-FEB-2001;

HSP RESEARCH INST INC
OS Mus Sp. (murine)
JP 2001054391-A/6
PD 27-FEB-2001
PF 11-NOV 1999 JP 1999321743
PF 11-NOV 1999 JP 1999321743
PF KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI TAKASHI YURA
PC C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00,C12N15/00,PC C12R1:91)
CC Key Location/Qualifiers
FT source 1.19
FT source 1.19
FT source 1.19
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               Endoplasmic reticulum stress transcription factor Patent: JP 2001054391-A 7 27-FEB-2001; HSP RESEARCH INST INC
                                                                                                                                           Rattus sp. Rattus sp.
                                                                                                                                                                         Endoplasmic reticulum stress transcription E44208 E44208.1 GI:18633461 JP 2001054391-A/7.
                                                            Haji, K., Yoshida, H., Mori, K., Yanagi, H. and Yura, T
                                                                                             Rattus
                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
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E44207.1 GI:18633460
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Endoplasmic reticulum stress
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                                                                                (bases 1 to 19)
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Rattus sp. (rat)
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8 c 5 g
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Pred. No. 1.8e+04;
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Pred. No. 1.8e+04;
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                                                                                                             Murinae;
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                                                                 Local Similarity
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CCAATCGCGCCGCACCACG
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PC C12N15/09,
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                                                                                                                                                                                                                                                                                                                        Patent: JP 2001054391-A 8 27-FEB-2001;
HSP RESEARCH INST INC
OS Homo sapiens (human)
PN JP 2001054391-A/8
PD 27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 19)
1 (bases 1 to 19)
1 Haji, K., Yoshida, H., Mori, K., Yanaqi, H. and Yura, T.
Endoplasmic reticulum Stress transcription factor
27-FFR-2001:
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                                                  Conservative
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27-FEB-2001
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/db_xref="taxon:9606"
10 c 4 g
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                                                                                                                                                                         Location/Qualifiers
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52.6%;
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                                                               Score 10; DB 6;
Pred. No. 1.8e+04
                                                                                                                                                                                     /organism='Homo sapiens (human)'.
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RESULT 18
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Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
Endoplasmic reticulum stress transcription factor
Patent: JP 2001054391-A 9 27-FEB-2001;
NT OS Gallus sp. (chicken)
PN JP 2001054391-A/9
PD 27-FEB-2001
PF 11-NOV-10^
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TAKASHI YURA
PC C12N15/0
(C12N15/00, P
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FH Key
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TAKASHI YURA
PC C12N15/09,(
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HSP RI
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                                                                                                                                                                                                                                                                                        E44211
E44211.1 GI:18633464
JP 2001054391-A/10.
                                                                                                                                                                                                                                                                                                                                    Endoplasmic reticulum stress transcription
                                                                                                                                                         Haji.K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T. Endoplasmic reticulum stress transcription factor Patent: JP 2001054391-A 10 27-FEB-2001; HSP RESEARCH INST INC
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 19)
                                                                                                                                                                                                                                                              Homo sapiens
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JP 2001054391-A/9.
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                              C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00
N15/00, PC C12R1:91)
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N15/00, PC C12R1:91)
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                                                                      KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI,
                                                                                                                                               Homo sapiens (human)
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                                                                                                     11-NOV-1999 JP 1999321743
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                                                                                                                  27-FEB-2001
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/db_xref="taxon:9036"
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1.8e+04;
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E44213.1 GI:18633466
JP 2001054391-A/12.
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Homo sapiens
                                               E44213
Endoplasmic reticulum
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Endoplasmic reticulum stress transcription
Patent: JP 2001054391-A 11 27-FEB-2001;
HSP RESEARCH INST INC
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                             /organism='Gallus sp.
Location/Qualifiers
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/db_xref="taxon:9036"
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/db_xref="taxon:9606"
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Pred. No.
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Pred. No.
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transcription
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1.8e+04;
                                                                                                                                                                                  1.8e + 04
                                                                                                                                                                                            DB 6;
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                                                                                                                                                                                                                                                                                           (chicken)'
                                               factor.
                                                           linear
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ORGANISM

Homo sapiens

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Local Similarity 52.6%;
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PN JP 2001054391-A/12
PD 27-EEB-2001
PF 11-NOV-1999 JP 1999321743
PR TAKASHI YURA
PC C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00,
                                                                                                                                       PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YA
TAKASHI YURA
PC C12N15/09,C12P21/02//(C12N15/09,C12R1:91),C12N15/00
(C12N15/00, PC C12R1:91)
CC C12R1:91)
FH Key Location/Qualifiers
FH source 1.19
FT /organism='Mus sp. (murine)'.
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PD
PD
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                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
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Mammalia; I
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                                                                                                                                                                                                                                                                                                               Mus sp. (murine)
JP 2001054391-A/13
27-FEB-2001
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                                             /organism="Mus sp."
/db_xref="taxon:10095"
6 c 6 g
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/db_xref="taxon:9606"
6 c 5 g
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   52.6%;
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Pred. No. 1.8e+04;
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CCAATATTACGTGACCACG 6
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                                                                                                                                                                                                                                                                   synthetic construct
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                                                                                                                                                                                                                               Gunderson, K.
                                                                                                                                                                                                                                                                              synthetic construct.
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/db_xref="taxon:32630"
/note="Computer Generated Probe Sequence."
5 c 9 g 7 t
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/db_xxef="taxon:32650"
/note="Computer Generated Probe Sequence."
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                                                             Score 10; DB 6;
Pred. No. 1.8e+04;
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Pred. No. 1.8e+04
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1 (bases 1 to 29)
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M10797
                                                                                                                                                                                                                                                                                                                                                       alpha-1 type III collagen.
                                                                                                                                                                   J. Biol. Chem. 260 (7), 4357-4363 (1985) 85157600
                                                                                                                                                                                                                l (bases 1 to 99)
Chu.M.L., Weil,D., de Wet,W., Bernard,M., Sippola,M. and Ramirez,F.
Isolation of cDNA and genomic clones encoding human pro-alpha 1
(III) collagen. Partial characterization of the 3' end region of
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                        Human DNA, libraries of A.Bank and T.Maniatis, clones IdF-[4,7].
                                                                                                                                                                                                                                                                                                                                                                        M10797.1 GI:180398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KYOSUKE HAJI, HIDEO YOSHIDA, KAZUTOSHI MORI, HIDEKI YANAGI, PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Artificial Sequence
JP 2001054391-A/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C12N15/09, C12P21/02//(C12N15/09, C12R1:91), C12N15/00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="synthetic construct"
                                                                                                        /organism="Homo sapiens"
                                                                                                                                     Location/Qualifiers
                                                                          /cell_type="fibroblast"
/codon_start=1
                /note="exon 22"
                                 /gene="COL3A1"
                                                              /tissue_lib="of
                                                                                          /db_xref="taxon:9606"
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Pred. No. 1.8e+04;
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                                                                  A.Bank and T.Maniatis"
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BASE COUNT
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Best Local Similarity 52.6%;
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                                                                                                                    76 CCAATCATCCTTTACCACG 94
                                                                                                                                                                                                 Local Similarity
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Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae YDL025W-A gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kumar, A., Harrison, P.M., Cheung, K.H., Lan, N., Echols, N., Bertone, P., Miller, P., Gerstein, M.B. and Snyder, M. An integrated approach for finding overlooked genes in yeast Nat. Biotechnol. 20 (1), 58-63 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces. 1 (bases 1 to 105)
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Kumar, A., Paul, H.M., Cheung, K.H., Lan, N., Echols, N., Bertone, P.,
Miller, P., Gerstein, M.B. and Snyder, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (01-FEB-2002) MCD Biology, Yale University, P.O. Box 208103, New Haven, CT 06520-8103, USA
112 bp
Sequence 1 from Patent WOO200706.
AX343726
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/protein_id="AAA51999.1"
/db_xref="GI:180411"
                                                                                                                                                                                                                                                                   /translation="MLMILWFFNQIARCRVNFTGGDGYKPIILYHVIH" 24 c 20 g 31 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Saccharomyces cerevisiae"
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                                                                                                                                                                                                                                                                                                                                                                 /gene="YDL025W-A"
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                                                                                                                                                                                                                                                                                                  /protein_id="AAL79254.1"
/db_xref="GI:18767078"
                                                                                                                                                                                                                                                                                                                                  /product="unknown"
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Pred. No. 1.8e+04;
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                                                                             Hideo,Y., Hideki,Y. and Takashi,Y.
Endoplasmic reticulum stress-response regulatory element
Patent: JP 199243959-A 4 14-SEP-1999;
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                                                                                                                                                                                                                                                                                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 122)
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                           TATA signal
                                                                                        enhancer
                                                                                                                    enhancer
                                                                                                                                                                         HIDEO YOSHIDA, HIDEKI YANAGI, TAKASHI YURA
C12N15/09, A61K35/74, A61K35/76, A61K38/00, A61K48/00, C12N15/C0,
                                                                                                        enhancer
                                                                                                                                          Topology: Linear;
                                                                                                                                                       Strandedness: Double;
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       /organism="Homo sapiens"
/db_xref="taxon:9606"
35 c 48 g 1
                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                       GI:13020854
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17 c 23 g 44 t
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/db_xref="taxon:115113"
<1. .111</pre>
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/db_xref="GI:18491805"
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/codon_start=1
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52.6%;
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116. .122.
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47.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                 80 CCAATCGGCGGCCTCCACG 98
                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                          1 CCAATNNNNNNNNCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 52.6%;
Local Similarity 52.6%;
  Unpublished
2 (bases 1
                        Blusch J.H., Deryckere, F., Windheim, M., Ruzsics, Z., Arnberg, N., Adrian, T. and Burgert, H.G.
E3/49K: A Novel Early Region 3 Protein Specifically Expressed By
                                                                 Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
1 (bases 1 to 125)
                                                                                                  human adenovirus type 19p.
human adenovirus type 19p
                                                                                                                                                                     Human adenovirus type 19p strain 587-partial sequence.
                                                                                                                                             AF271990.1 GI:14279590
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(C12N15/00, PC
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PD
PF
PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endoplasmic reticulum stress transcription factor Patent: JP 2001054391-A 4 27-FEB-2001; HSP RESEARCH INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PI KYOSUKE HAJI,HIDEO YOSHIDA,KAZUTOSHI MORI,HIDEKI YANAGI, PI
TAKASHI YURA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Haji,K., Yoshida,H., Mori,K., Yanagi,H. and Yura,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homon (bases 1 to 122)
(bases 1 to 125)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E44205.1 GI:18633458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endoplasmic reticulum stress transcription factor.
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                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
JP 2001054391-A/4
27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NOV-1999 JP 1999321743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism='Homo sapiens (human)'.
                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                 52.6%;
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Pred. No. 1.8e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Pred. No. 1.8e+04;
Pred. No. 1.8e+04;
                                                                                                                                                                                               125 bp
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                                                                                                                                                                                               DNA
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                                                                                                                                                                           inverted terminal repeat,
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                                                                                                                                                                                                                                                                                                              0;
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BASE COUNT
ORIGIN
Search completed: November 16, 2002, 02:59:16 Job time: 2579 secs
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                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
                                                                                                       Query Match 52.6%; Score 10; DB 14; Length 125; Best Local Similarity 52.6%; Pred. No. 1.8e+04; Matches 10; Conservative 0; Mismatches 9; Indels
                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                              source
                                                    86 CCAATCAACGACGACCACG 68
                                                                   1 CCAATNUNUNUNUNCCACG 19
                                                                                                                                                                                                                                                                                                      Ruzsics, Z. and Burgert, H.G.

Direct Submission

Submitted (25-MAY-2000) Dep. of Virology, Gene Center-Max v.

Pettenkofer Inst., Feodor-Lynen-Str. 25, Muenchen 81377, Germany
Location/Qualifiers
                                                                                                                                                                          43 a
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// SIDS2/gcgdata/geneseq/Jeneseqn.embl/NA20UE	N_Geneseq_101002:*    SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*   SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*	nber of hi	Title: US-09-606-804-1  perfect score: 19	GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.  Copyright (c) 1	Mon Nov 18 08:09:24 2002
10 52.6 294 2 10 52.6 294 2 10 52.6 306 1 10 52.6 306 1 10 52.6 306 1 10 52.6 306 3 10 52.6 308 3 10 52.6 313 3 10 52.6 328 3 10 52.6 338 3 10 52.6 360 3	42 10 52.6 14.3 21 AAA71907 43 10 52.6 14.5 22 AAF67488 43 10 52.6 14.5 22 AAF71910 45 10 52.6 150 21 AAA71909 45 10 52.6 150 21 AAA71909 46 10 52.6 155 24 ABN01584 c 47 10 52.6 210 24 ABN01584 c 50 10 52.6 210 24 AAA0353 c 51 10 52.6 220 24 ABN26353 c 51 10 52.6 220 24 ABN26353 c 52 10 52.6 220 24 ABN26353 c 53 10 52.6 220 24 ABN26342 c 54 10 52.6 237 22 AAS24832 c 54 10 52.6 237 22 AAS24832 c 55 10 52.6 261 22 AAF17718 55 10 52.6 261 22 AAF17718 56 10 52.6 261 24 ABN25333 c 58 10 52.6 263 24 ABN25333 c 58 10 52.6 263 24 ABN25333 c 58 10 52.6 268 22 ABN11677 c 59 10 52.6 272 27 ABS949758 c 60 10 52.6 272 27 AAS59493	10 52.6 29 21 10 52.6 30 21 10 52.6 33 21 10 52.6 112 24 10 52.6 122 21 10 52.6 122 21 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24 10 52.6 123 24	10. 52.6 24 24 10 52.6 24 24 10 52.6 24 24 10 52.6 24 24 10 52.6 25 19 10 52.6 25 24 24 10 52.6 25 24 21 10 52.6 25 24 21 10 52.6 25 24 21 10 52.6 25 24 21 10 52.6 25 24 21 10 52.6 28 21 10 52.6 28 21	2.6 19 21 2.6 19 21 2.6 19 21 2.6 19 21 2.6 19 21 2.6 19 21 2.6 19 21 2.7 19 21 2.7 19 21 2.7 19 21 2.7 19 21 2.7 19 21 2.7 22 2.7 19 21 2.7 22 2.7 2	0 10 52.6 19
Corn Lassetz Conn Human ORF4323 Aylanase gene frag Xylanase gene frag Aylanase clausii g Bacillus clausii g Bacillus clausii g Bacillus clausii g Human ORFX polynuc Human prostate exp Human prostate tum Human brain Expres Human ovarian tumo DNA encoding novel Sequence encoding Sequence encoding Glucose regulated Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia DNA encoding cancer Human colon cancer Human colon cancer	Novel human pulying rayment NS fr IAK fragment relation according to the property of the pro	GRP94 PLONGER TAN GRP78 promoter tan GRP78 promoter Human GRP78 promot 5' flanking region * Human ovarian canc Human ovarian canc Ink fragment NS fr Ink fragment NS fr Ink fragment NS fr	Oligonucleotide ad oligonucleotide ERS GRP94 promoter ERS GRP94 promoter ERS	GRP78 promoter ERS GRP94 promoter ERS GRP96 promoter ERS ENSE1 consensus see ERSE1 consensus see ERSE2 consensus see ERSE2 consensus see ERSE3 consensus see ERSE3 consensus see ERSE3 consensus see ERSE3 consensus see ERSE4 consensus see ERSE5 consensus see ERSE6 consensus see ERSE6 consensus see ERSE7 consensus see ERSE6 consensus see ERSE7 consensus see ERSE6 consensus see ERSE6 consensus see ERSE7 consensus see ERSE6 consensus see ERSE6 consensus see ERSE7 consensus	1.

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83 84 85 86 87 88 89

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AAZ25632 standard; DNA; 19
                                                                                                                                                                                         The present invention specifically claims an element shown by: (A) a sequence having replaced 1-3 bases with the other base(s), which induces competence of endoplasmic reticulum. Also described are: (1) a DNA induces containing the above mentioned element, optionally further containing a ctivity with stress on endoplasmic reticulum. Also described are: (1) a DNA having promoter DNA; and (2) a vector containing the element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation.
                                                                                                                                                                                    Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;
                                                                                                1 CCAATNUNNNNNNNCCACG 19
                                                                                                                      1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 10; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-603708/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HSPK-) HSP KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cystic fibrosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Endoplasmic reticulum, ER, stress competence; control element,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endoplasmic reticulum stress competence control element SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ25631 standard; DNA; 19 BP.
                                                                                                                                                               Similarity
                                                                                                                                                  Conservative
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                                                                                                                           100.08; Preu. ...
tive 0; Mismatches
                                                                                                                                                                         52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis; cancer; autoimmune disease;
                                                                                                                                                  Score 10; DB 20;
, Pred. No. 1.4e+0;
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AAS90032
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AAH65636
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                                                                                                                                               1.4e+03;
                                                                                                                                  0; Indels
                                                                                                                                                       Length 19;
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JP11243959-A.
                        Mus sp.
                         Endoplasmic reticulum; ER; Stress competence; control element;
inhibition; growth; apoptosis; cancer; autoimmune disease;
cystic fibrosis; ds.
                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                   Query Match
                                                             Endoplasmic reticulum stress competence control element SEQ ID NO:6.
                                                                                                                    23-DEC-1999
                                                                                                                                              AAZ25633;
                                                                                                                                                         AAZ25633 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                    1 CCAATCGGCGGCCTCCACG 19
                                                                                                                                                                                                                                         1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                        Local Similarity es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New control element for stress competence of endoplasmic reticulum useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-603708/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HSPK-) HSP KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endoplasmic reticulum stress competence control element SEQ ID NO:5.
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                                                                                                           (first entry)
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                              52.6%;
52.6%;
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                                                                                                                                                                                                                                                                                  Score 10;
                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                    1.4e+03;
9;
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RESULT 2 AAZ25632

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Matches Query Match

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New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
                                                     WPI; 1999-603708/52
                                                                               (HSPK-) HSP KENKYUSHO KK
                                                                                                               04-MAR-1998;
                                                                                                                                         04-MAR-1998;
                                                                                                                                                                       14-SEP-1999.
                                                                                                                                                                                                                                                                             Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                                                                                                      Endoplasmic reticulum stress competence control element SEQ ID NO:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
                                                                                                                                                                                                  JP11243959-A
                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                           cystic tibrosis; ds
                                                                                                                                                                                                                                                                            inhibition;
                                                                                                                                                                                                                                                                                                                                               23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                            AAZ25634;
                                                                                                                                                                                                                                                                                                                                                                                                   AAZ25634 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention specifically claims an element shown by: (A) a 19 bb base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCAATCGGAGGCCTCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                 growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                              98JP-0052453
                                                                                                                                      98JP-0052453.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.6%;
52.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Вb
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The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic containing a promoter DNA; and (2) a vector containing the above mentioned element, optionally further optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of
                                                                                                                                                                                                                                                useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                 New control element for stress competence of endoplasmic reticulum
                                                                                                                                                                                                          Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                              WPI; 1999-603708/52
                                                                                                                                                                                                                                                                                                                                                                               04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                             (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cystic fibrosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endoplasmic reticulum; ER; stress competence; control element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Endoplasmic reticulum stress competence control element SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention specifically claims an element shown by: (A) a 19 bb base sequence, CCAATNUNNU NUNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces competence of endoplasmic reticulum. Also described are: (1) a DNA reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element containing the behaving transcription of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. ARZ25632 to ARZ25657 represent elements used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ25635 standard; DNA; 19 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inhibition; growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 3; 25pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
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AAZ25636
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                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autoantibody formation. AA225632 to AAZ25657 represent elements used in
                                                                                                                                                                   The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA competence of inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element of optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic reticulum stress competence control element SEQ ID NO:9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ25636 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                             New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-1998;
                                                                                                                         sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                 CELIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-603708/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                         an example from the present invention.
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Local Similarity 52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CCAATUNNUNUNUNCCACG 19
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 1 CCAATGGGAGCGCACCACG 19
                                1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    growth; apoptosis; cancer; autoimmune disease;
                                                                Conservative
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                                                                               52.6%;
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Pred. No. 1.4e+03;
                                                                   0;
                                                                                 Score 10; DB 20;
Pred. No. 1.4e+03;
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                                                                   Mismatches
                                                                      9.
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                                                                      Indels
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RESULT 7
AAZ25637
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATINNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element of optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in an example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cystic fibrosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New control element for stress competence of endoplasmic reticulum useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-603708/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HSPK-) HSP KENKYUSHO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;
                                                                                                                                                                                         AAZ25538 standard; DNA; 19 BP
              inhibition; growth; apoptosis; cancer; autoimmune disease; cystic fibrosis; ds.
                                                                                  Endoplasmic reticulum stress competence control element SEQ ID NO:11.
                                                                                                                                                          AAZ25638;
                                             Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                       23-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                             1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                              1 CCAATCGGAAGGAGCCACG 19
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                                                                                                                       (first entry)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                          1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                          DB 20;
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        WPI; 1999-603708/52
                              (HSPK-) HSP KENKYUSHO KK
                                                           04-MAR-1998;
                                                                                 04-MAR-1998;
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                                                                                                          14-SEP-1999.
                                                                                                                                                           Homo sapiens
                                                                                                                                                                                   cystic fibrosis; ds
                                                                                                                                                                                                 Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                      Endoplasmic reticulum stress competence control element SEQ ID NO:12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                having transcription inducing activity with stress on endoplasmic reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
                                                                                                                                                                                                                                                             23-DEC-1999
                                                                                                                                                                                                                                                                                        AAZ25639;
                                                                                                                                                                                                                                                                                                          AAZ25639 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 19 BP; 4 A; 9 C; 5 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNNNNN NNNNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces transcription with stress on endoplasmic reficulum used for stress competence of endoplasmic reficulum. Also described are: (I) a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 3; 25pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                              1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                             ibition; growth;
                                                                                                                                                                                                                                                                                                                                                                       1 CCAATCGACGCCGGCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                        ocal Similarity
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                                                                                                                                                                                         apoptosis; cancer; autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                    52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 10; DB 20, Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 19;
                                                                                                                                                                                       disease;
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RESULT 10
AAZ25640
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The present invention specifically claims an element shown by: (A) a 19 bb base sequence, CCAATNNNN NNNNCCACG (ERRE); or (B) a modified base sequence having replaced 1-3 bases with the other base(S), which induces transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element
                                                                                                                                                               Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                    New control element for stress competence of endoplasmic reticulum - useful for inhibition of growth and induction of apoptosis in cancer
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                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                          JP11243959-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cystic fibrosis; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Endoplasmic reticulum; ER; stress competence; control element;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic reticulum stress competence control element SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ25640 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAZ25640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               reticulum containing the above mentioned element, optionally further containing a promoter DNA; and (2) a vector containing the element optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZ25632 to AAZ25657 represent elements used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19 BP; 5 A; 6 C; 5 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     transcription with stress on endoplasmic reticulum used for stress competence of endoplasmic reticulum. Also described are: (1) a DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention specifically claims an element shown by: (A) a 19 bp base sequence, CCAATNUNUN NUNUNCCACG (ERSE); or (B) a modified base sequence having replaced 1-3 bases with the other base(s), which induces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New control element for stress competence of endoplasmic reticulum useful for inhibition of growth and induction of apoptosis in cancer \overline{\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   having transcription inducing activity with stress on endoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 3; 25pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CCAATGATGGTCGACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth; apoptosis; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                       98JP-0052453
                                                                                                                                                                                                                                                                                                                                                                      98JP-0052453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 1.4e+03;
tches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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9999998<del>x</del> &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              optionally with the DNA. The element can be used for the inhibition of growth and induction of apoptosis of cancer cells, and improvement of symptoms of autoimmune diseases and cystic fibrosis by inhibition of autoantibody formation. AAZZ5632 to AAZZ5657 represent elements used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA28570 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GRP78 promoter ERSE1-like sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA28570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; human; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic reticulum; stress; ER; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2000 (first entry)
                                                                                                                                                    An endoplasmic reticulum stress transcription factor (bZIP) an capable of regulating transcription inducing activity exhibited by an capable of regulating transcription inducing activity exhibited by an endoplasmic reticulum chaperone. The method comprises expressing an endoplasmic reticulum chaperone The method comprises expressing bzIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of chaperone gene. bZIP is useful for controlling the expression of chaperone gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1999;
                          endoplasmic reficulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reficulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP78 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                    New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-387736/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HSPR-) HSP RES INST INC
                                                                                                                                                                                                                                                                                                      Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                        diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                       for treating cancers, arteriosclerosis, cystic fibrosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCAATUNNUNUNUNCCACG 19
                 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAATGAGGGTCGACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99JP-0163112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0324227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP06305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ВΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 score 10; DB 20;
pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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RESULT 12
AAA28571
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Дb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                              An endoplasmic reticulum stress transcription factor (bZIP) and ccapable of regulating transcription inducing activity exhibited by an CC capable of regulating transcription inducing activity exhibited by an CC element (ERSE) can be used in a method for controlling expression of CC an endoplasmic reticulum chaperone. The method comprises expressing CC bZIP. The method can be used for expression of a foreign protein by CC positively regulating expression of an endoplasmic reticulum consperone either positively or negatively in CC central and therefore is useful for treatment or prophylaxis of CC central and therefore is useful for treatment or prophylaxis of CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, the CC expression of a foreign protein. This sequence taken from the CC expression of a foreign protein (GRP) promoter GRP78 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 3 A; 9 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA28571 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression; GRP; glucose regulated protein; promoter; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse; cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRP78 promoter ERSE1-like sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA28571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HSPR-) HSP RES INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haze K. Yoshida H.
                                                                                                                                                                                                                                                                                                                              Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-387736/33.
                                                                                                                                                                                                                                                                                                                                                                   diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCAATCGGCGGCCTCCACG 19
Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-0324227.
99JP-0163112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-JP06305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10; DB 21;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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Matches

10;

Conservative

0;

Mismatches No.

Query Match Best Local Similarity

52.6%;

Pred.

1.4e+03;

DB 21;

Length 19; Indels

0

Gaps

0;

Score 10;

Š В

RESULT 13

AAA28572 standard; DNA; 19 BP

GRP78 promoter ERSE1-like sequence.

29-AUG-2000 (first entry)

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Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; rat; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             An endoplasmic reticulum stress transcription factor (b2IP) an capable of regulating transcription inducing activity exhibited by an capable of regulating transcription inducing activity exhibited by an endoplasmic reticulum chaperone. The method comprises expressing an endoplasmic reticulum chaperone. The method comprises expressing b2IP. The method can be used for expression of a foreign protein by b2IP. The method can be used for expression of an endoplasmic reticulum positively regulating expression of an endoplasmic reticulum chaperone gene. b2IP is useful for controlling the expression of chaperone gene. b2IP is useful for controlling the expression of
                                                                                                                                                                                                                                                                                           endoplasmic reticulum chaperone either positively or negatively in endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the expression of a foreign protein (GRP) promoter GRP78 contains an ERSE lightcose regulating protein (GRP) promoter GRP78 contains an ERSE lightcose regulating protein (GRP) promoter GRP78 contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endoplasmic reticulum stress transcription factor (known as bZIP) controlling expression of endoplasmic reticulum chaperone, useful treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                        contains an ERSE like
                                                                                                                                                       Gaps
                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA28573
ID AAA2
                                                                                                                                                                                                                                                                                                                                                                                                                В
                                                                                                                    AAA28574
                                                                                                                                            RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression; GRP; glucose regulated protein; promoter; Ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Endoplasmic reticulum; stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRP94 promoter ERSE1-like sequence.
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cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An endoplasmic reticulum stress transcription factor (bZIP) an capable of regulating transcription inducing activity exhibited by an capable of regulating transcription inducing activity exhibited by an endoplasmic reticulum chaperone. The method comprises expressing an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by bZIP. The method can be used for expression of a foreign protein by chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in endoplasmic reticulum chaperone either positively or negatively in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haze K, Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HSPR-) HSP RES INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-387736/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the endoplasmic reticulum chaperone and thereby increases the the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP94 contains an ERSE like glucose regulating protein (GRP) promoter GRP94.
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 19 BP; 4 A; 10 C; 4 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence
29-AUG-2000
                                               AAA28574;
                                                                                               AAA28574 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                   1 CCAATCGCGCCGCACCACG 19
                                                                                                                                                                                                                                                                   1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0324227.
99JP-0163112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-JP06305
       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mori K,
                                                                                                                                                                                                                                                                                                                                                     52.6%;
                                                                                                            ВΡ
                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yanagi H,
                                                                                                                                                                                                                                                                                                                                                     Score 10; I
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yura T;
                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                .4e+03;
                                                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                0
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WPI; 2000-387736/33

Haze K,

Yoshida H, Mori K,

Yanagi H,

Yura T;

Example 1; Fig 3; 157pp; English. diseases, wounds and ulcers 09-JUN-1999;

13-NOV-1998; 12-NOV-1999;

98JP-0324227 99JP-0163112 99WO-JP06305

(HSPR-) HSP RES INST INC.

25-MAY-2000 WO200029429-A2 Rattus rattus.

δÕ В

1 CCAATNNNNNNNNCCACG 19 CCAATCGGAGGCCTCCACG 19

Query Match

Local Similarity

Sequence 19 BP; 4 A; 8 C; 5 G; 2 T; 0 other;

Matches

10;

Conservative

0;

52.6%; 52.6%;

Score 10; Pred. No. Mismatches

1.4e+03;

Indels

0;

DB 21; Length 19;

Gaps

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AAA28575
                                                                                                                                                                                                                                                                                                                                                                                                                 В
                                                                                                                                                                                                                                                                                                                                                                                                                                                    An endoplasmic reticulum stress transcription factor (bZIP)
C capable of regulating transcription inducing activity exhibited by an CC element (ERSE) can be used in a method for controlling expression of CC an endoplasmic reticulum chaperone. The method comprises expressing CC positively regulating expression of a nedoplasmic reticulum chaperone of a foreign protein by CC chaperone gene. bZIP is useful for controlling the expression of cendoplasmic reticulum chaperone either positively or negatively in CC cells and therefore is useful for treatment or prophylaxis of CC cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, CC the endoplasmic reticulum chaperone and thereby increases the CC cancers of a foreign protein. This sequence taken from the correct conformation of CC capression of a foreign protein. This sequence taken from the
                                                                                                                                                                                                                                                                                                                                               Matches
       Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
   prophylaxis; cancer; arteriosclerosis; ischaemia;
                                                                          GRP94 promoter ERSE3-like sequence.
                                                                                                               29-AUG-2000 (first entry)
                                                                                                                                                                               AAA28575 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19 BP; 5 A; 7 C; 6 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                       glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-387736/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                   1 CCAATGGGAGCGCACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1999;
                                                                                                                                                                                                                                                                                                  1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus domesticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRP94 promoter ERSE1-like sequence.
                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshida H,
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0324227.
99JP-0163112.
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                                                                                                                                                                                                                                                                                                                                                   52.6%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mori K,
                                                                                                                                                                                                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                        Score 10; DB 21;
Pred. No. 1.4e+03;
""Armatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yanagi H, Yura T;
                                                                                                                                                                                                                                                                                                                                                        Length 19;
wound healing;
                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                    0;
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WO200029429-A2

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                                                                                                                                                                                                                                                                                                                                                    Qy
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Ad
XX
XX
XX
Nd
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                  Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatme prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene; chicken;
                        Gallus domesticus
                                     gene expression; GRP; glucose regulated protein; promoter;
                                                                                                                                        GRP94 promoter ERSE3-like sequence.
                                                                                                                                                                       29-AUG-2000 (first entry)
                                                                                                                                                                                                               AAA28576;
                                                                                                                                                                                                                                      AAA28576 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 6 A; 6 C; 6 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endoplasmic reticulum chaperone either positively or negatively in ceils and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glucose regulating protein (GRP) promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of regulating transcription inducing activity exhibited by element (ERSE) can be used in a method for controlling expression o an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               An endoplasmic reticulum stress transcription factor (bZIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HSPR-) HSP RES INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cystic fibrosis; ulcer; gene therapy; recombinant gene; human; gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                                                                                        H
                                                                                                                                                                                                                                                                                                                                          1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W0200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eomo sapiens.
                                                                                                                                                                                                                                                                                                            CCAATCGGAAGGAGCCACG 19
                                                                                                                                                                                                                                                                                                                                                                              10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0163112
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                                                                                                                                                                                                                                                                                                                                                                                      52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mori K,
                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     Score 10;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                 .4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRP94 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                               Length 19;
                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                   treatment;
                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 18
AAA28577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP94 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of
 13-NOV-1998;
                                                                                                                                                       prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing;
cystic fibrosis; ulcer; gene therapy; recombinant gene; human;
gene expression; GRP; glucose regulated protein; promoter; ss.
                                                                                                                                                                                                                                                       Calreticulin promoter ERSE3-like sequence.
                                                                                                                                                                                                                                                                                                                                                    AAA28577 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                    Endoplasmic reticulum; stress; ER; transcription factor;
transcription; regulatory element; ERSE; bZIP; chaperone; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    capable of regulating transcription inducing activity exhibited by element (ERSE) can be used in a method for controlling expression c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-387736/33.
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                                 12-NOV-1999;
                                                                                              WO200029429-A2
                                                                                                                                                                                                                                                                                        29-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An endoplasmic reticulum stress transcription factor (bZIP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2000
                                                                25-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCAATCGACGCCGGCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAATUNNUNUNUNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endoplasmic reticulum stress transcription factor (known as bZIP) controlling expression of endoplasmic reticulum chaperone, useful treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                            sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSP RES INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP; 4 A; 9 C; 5 G; 1 T; 0 other;
                                                                                                                                                                                                                                                                                       (first entry)
                                 99WO-JP06305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99JP-0163112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.6%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 10; DB 21;
Pred. No. 1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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RESULT 19
AAA28578
ID AAA28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by a element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in
                                                                                                                                                                                                                                                                 Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; trea prophylaxis; cancer; arteriosclerrosis; ischaemia; wound healin cystic fibrosis; ulcer; gene therapy; recombinant gene; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the calreticulin (CRT) promoter contains an ERSE like sequence.
                            Haze K,
                                                                                     13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                            Calreticulin promoter ERSE3-like sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA28578 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases,
                                                                                                                                   12-NOV-1999;
                                                                                                                                                                                            W0200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wounds and ulcers. bZIP also maintains the correct conformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Fig 3; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-387736/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HSPR-) HSP RES INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-JUN-1999;
                                                         (HSPR-) HSP RES INST INC
                                                                                                                                                               25-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                           29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity es 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CCAATGATGGTCGACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCAATUNNUNUNUCCACG 19
                                                                                                                                                                                                                                                      expression;
                            Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 5 A; 6 C; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                     98JP-0324227
99JP-0163112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99JP-0163112.
                                                                                                                                 99WO-JP06305
                                                                                                                                                                                                                                                     GRP; glucose regulated protein; promoter; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52.6%;
                            Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yanagi H,
                            Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 21;
                          Yura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Т;
                             Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                               chaperone; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                 healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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on of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (ERSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the
                                           New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                                                                                                                                                                                                                                                              Endoplasmic reticulum; stress; ER; transcription factor; transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene;
                                diseases, wounds and ulcers
                                                                                                                                                                                                                         13-NOV-1998;
09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                 WO200029429-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA28680 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases, wounds and ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                        (HSPR-) HSP RES INST INC
                                                                                                                                                                                                                                                                              12-NOV-1999;
                                                                                                                                                                                                                                                                                                                25-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERSE1 consensus sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19 BP; 5 A; 6 C; 6 G; 2 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         calreticulin (CRT) promoter contains an ERSE like sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CCAATNNNNNNNNNCCACG 19
                                                                                                                      2000-387736/33
                                                                                                                                                                                                                                                                                                                                                                                                               expression; GRP; glucose regulated protein; promoter; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAATGAGGGTCGACCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                     Yoshida H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                         98JP-0324227
99JP-0163112
                                                                                                                                                                                                                                                                            99WO-JP06305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.6%;
52.6%;
                                                                                                                                                       Mori K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 10; DB 21;
Pred. No. 1.4e+03;
                                                                                                                                                     Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                     Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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Claim 1;

Page 130; 157pp; English

Sequence 19 BP; 3 A; 5 C; 1 G;

1 T;

9 other

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                              The present invention relates to a method for screening a substance for controlling ORP150 expression. The method comprises examining the expression of a reporter gene product in the presence of a cell strain transformed by a vector. In the vector, the reporter gene is connected downstream of the promotor region of ORP150 gene and a sample to be tested. The method can be used to obtain drug compositions which alter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (BRSE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bZIP The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum chaperone gene. bZIP is useful for controlling the expression of endoplasmic reticulum chaperone either positively or negatively in
                                                                         various diseases e.g. ischaemic diseases, wounds, ulcers, diabetes, neurodegenerative diseases, cancers or autoimmune diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bZIP also maintains the correct conformation of
                                                       sequence is an ERSE consensus sequence which was used in an example from
                                                                                                            ORP150 expression. The drug composition can be used for the treatment of
                                                                                                                                                                                                                                                                       Example 3; Page 9; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                  Screening a substance for controlling ORP150 expression,
                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-610059/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2000; 2000JP-0055384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2000; 2000JP-0055384.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORP150; drug; ischaemic disease; wound; ulcer; diabetes; ERSE; neurodegenerative disease; cancer; autoimmune disease; promoter; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;
                                                                                                                                                                                                                                                                                                                                  produce drugs for the treatment of diseases associated with ORP150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP20(1238699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERSE consensus sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAI7(0001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAI7(001 standard; DNA; 19 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein.
                                                                                                                                                                                                                                                                                                                                                                                                                               (HSPK-) HSP KENKYUSHO KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCAATNUNNNNNNNCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CCAATNUNNNNNNCCACG 19
                                    present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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Targeted gene expression is tool used for gene therapy of diseases and CC is based on 2 main strategies: (1) targeted entry of a heterologous CC nucleic acid to a host cell; and (2) specific tissue or cell expression CC of the heterologous gene. In general, heterologous gene expression CC general purpose Murine Leukaemia Virus (MuLV) Long Terminal Repeat (LTR) CC promoter sequence. Promoters such as these sometimes fail to adequately CC express the heterologous gene in a biologically stressed environment. CC at least one stress-responsive non-coding regulatory sequence comprising CC at least two copies of an endoplasmic reticulum stress element (ERSE). CC The preferred ERSE of the invention is the sequence shown here which cC corresponds to a glucose responsive protein (grp) 78 gene promoter ERSE. CC The construct also comprises a heterologous nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF28780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                               A nucleic acid construct comprises a stress-responsive non-coding regulatory sequence useful in treating and detecting cell proliferative disorders, e.g. cancer, or biological stress resulting from glucose
                                                                                                                                                                                                                                Claim 1; Page 83; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                        WPI; 2001-071484/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                             (UYSC-) UNIV SOUTHERN CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                               28-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-2000; 2000WO-US17885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200100791-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; antidiabetic; dermatological; hepatotropic; gene therapy, heterologous gene expression; stress-responsive regulatory sequence; endoplasmic reticulum stress element; ERSE; glucose responsive protein; grp78; promoter; cell proliferative disorder; inflammation; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diabetes; human; transgenic animal; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endoplasmic response stress element motif.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF28780 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF28780,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCAATNNNNNNNNNCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0141505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
15..19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /bound_moiety= "YY1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /bound_moiety= "CBF/NF·Y proteins"
6..14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "GC-rich region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 19;
1.4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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ACCCCCCXXX PXX PT PT PT XX PXX PT XX PT XX

An endoplasmic reticulum stress transcription factor (bZIP) capable of regulating transcription inducing activity exhibited by an element (EREE) can be used in a method for controlling expression of an endoplasmic reticulum chaperone. The method comprises expressing bZIP. The method can be used for expression of a foreign protein by positively regulating expression of an endoplasmic reticulum

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AAA28596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                             New endoplasmic reticulum stress transcription factor (known as bZIP) for controlling expression of endoplasmic reticulum chaperone, useful
Example 1; Fig 7; 157pp; English.
                                                      for treating cancers, arteriosclerosis, cystic fibrosis, ischemic
                                                                                                                                                                                WPI; 2000-387736/33.
                                                                                                                                                                                                                                                                        (HSPR-) HSP RES INST INC
                                                                                                                                                                                                                                                                                                                           09-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W0200029429-A2
                                                                                                                                                                                                                                                                                                                                                     13-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unspecified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transcription; regulatory element; ERSE; bZIP; chaperone; treatment; prophylaxis; cancer; arteriosclerosis; ischaemia; wound healing; cystic fibrosis; ulcer; gene therapy; recombinant gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           operatively linked to the regulatory sequence, where expression of the heterologous sequence is regulated by the non-coding sequence and where the heterologous sequence encodes a therapeutic agent effective for provided a cell proliferative disorder or for treating a disorder or associated with glucose starvation or a detectable marker. The invention possibly associated with inflammation, for example meoplastic disorders such as lung cancer, colon-rectum cancer, breast cancer, prostate cancer, urinary tract cancer, uterine cancer lymphoma, oral cancer, pancreatic brain cancer and ovarian cancer. The invention is also useful for cancer, colon-human transgenic animals of the invention is also useful for cancer.

Non-human transgenic animals of the invention include vertebrates such as any colon-human primary enters such as diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endoplasmic reticulum; stress; ER; transcription factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRP78 promoter ERSE1-like sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19 BP; 3 A; 5 C; 1 G; 1 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as rodents, non-human primates, sheep, dogs, cows, pigs, amphibians,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAATNNNNNNNNCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression; GRP; glucose regulated protein; promoter; ss
                                                                                                                                                                                                                            Yoshida н,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                 Yanagi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                 Yura T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .4e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the endoplasmic reticulum chaperone and thereby increases the expression of a foreign protein. This sequence taken from the glucose regulating protein (GRP) promoter GRP/8 contains an ERSE like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endoplasmic reticulum chaperone either positively or negatively in cells and therefore is useful for treatment or prophylaxis of cancers, arteriosclerosis, cystic fibrosis, ischaemic diseases, wounds and ulcers. bzlp also maintains the correct conformation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chaperone gene. bZIP is useful for controlling the expression of
Matches
                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 5 A; 10 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oligonucleotide array; adapter sequence; probe; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oligonucleotide adapter/capture probe 191.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ00200 standard; DNA; 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ00200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200216649-A2.
                                                                                                  The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in AB000010-AB013409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (AB000010-AB013409) to a target nucleic acid to form a modified target (AB000010-AB013409) to a target nucleic acid to form a modified with (I). nucleic acid and contacting the modified target nucleic acid with (I) the steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-AUG-2001; 2001WO-US26519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2002
                                                                                                                                                                                                                                                                                                      Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                                                                                                                                       Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2000; 2000US-228854P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-AUG-2000; 2000US-227948P
                                                                                                                                                                                                                                                           Claim 1; Page 48; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                            different specific capture probes
                                                        Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
                                                                                        nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 CCAATCGGCGGCCTCCACG 23
             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
   10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
Conservative
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52.6%;
                  52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10; DB 21;
Pred. No. 1.5e+03;
      0,
                    Score 10; DB 24;
Pred. No. 1.5e+03
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     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                    DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
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          9
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                                      Length 24;
           Indels
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             0,
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RESULT 25
ABQ04398/c
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 XXX DXX AC
                                                                                                                      ABQ04439
                                                                                                                                RESULT 26
                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                            Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABQ04398 standard; DNA; 24 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide adapter/capture probe 4389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                   25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid and target nucleic acid with (I). nucleic acid and contacting the modified target nucleic acid with (I). The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target which further comprises detecting the presence of the modified target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gunderson K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-AUG-2000; 2000US-22/948P
29-AUG-2000; 2000US-228854P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 144; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 CCAATATTACGTGACCACG 5
                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an oligonucleotide array (I) comprising at least
                                                                                                                                                                                                                                                                                 Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                            nucleic acid.
Oligonucleotide array; adapter sequence; probe; ss.
                          Oligonucleotide adapter/capture probe 4430.
                                                                                                         ABQ04439 standard; DNA; 24 BP
                                                     11-JUN-2002
                                                                                                                                                                         23 CCAATATTACGTGACCACG
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                     1 CCAATNUNUNUNUNCCACG 19
                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000US-227948P
                                                        (first entry)
                                                                                                                                                                                                                                               52.6%;
                                                                                                                                                                                                                                            Score 10; DD - NO. 1.5e+03;
                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                 Length 24;
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RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                    Matches
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       Gunderson K;
                                               25-AUG-2000; 2000US-227948P.
29-AUG-2000; 2000US-228854P.
                           (ILLU-) ILLUMINA INC
                                                                                 27-AUG-2001; 2001WO-US26519.
                                                                                                             28-FEB-2002
                                                                                                                                                                    Oligonucleotide array; adapter sequence; probe; ss
                                                                                                                                     WO200216649-A2
                                                                                                                                                                                             Oligonucleotide adapter/capture probe 10676
                                                                                                                                                                                                                         11-JUN-2002 (first entry)
                                                                                                                                                                                                                                                      ABQ10685;
                                                                                                                                                                                                                                                                     ABQ10685 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a adapter nucleic acid (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). which further comprises detecting the presence of the modified target nucleic acid, which further comprises detecting the presence of the modified target
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 144; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-AUG-2000; 2000US-227948P.
29-AUG-2000; 2000US-228854P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-AUG-2001; 2001WO-US26519
                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                               2 CCAATATTACGTGACCACG 20
                                                                                                                                                                                                                                                                                                                                                    1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                      52.6%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                              Score 10;
                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      No.
                                                                                                                                                                                                                                                                                                                                                                                  1.5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                           Length 24;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                Claim 1; Page 221; 261pp; English.
                                                                                                                                                                               different specific capture probes
                                                                                                                                                                                 Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
                                                                                                                                                                                                                                                  WPI; 2002-292068/33.
                                                                                                                                                                                                                                                                                   Gunderson K;
                                                                                                                                                                                                                                                                                                                                       25-AUG-2000; 2000US-227948P.
29-AUG-2000; 2000US-228854P.
                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2001; 2001WO-US26519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide array; adapter sequence; probe; ss.
                                                                                                                                                                                                                                                                                                           (ILLU-) ILLUMINA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                 W0200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oligonucleotide adapter/capture probe 10717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABQ10726 standard; DNA; 24 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target (ABQ00010-ABQ13409) to a target nucleic acid to form a modified target nucleic acid and contacting the modified target nucleic acid with (I). Which further comprises detecting the presence of the modified target nucleic acid, which further comprises detecting the presence of the modified target nucleic acid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24 BP; 4 A; 5 C; 9 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an oligonucleotide array (1) comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 221; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Array comprising adapter sequences useful for immobilizing or detecting a target nucleic acid sequence, has different addresses comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 CCAATATTACGTGACCACG 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%;
52.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 10;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .5e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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SSSSS

nucleic acid

Sequence 24 BP; 6 A; 9 C; 5 G; 4 T; 0 other;

which further comprises detecting the presence of the modified target

Qy

1 CCAATNUNNNNNNNCCACG 19

2 CCAATATTACGTGACCACG 20

Matches Query Match

10;

Conservative

0; Pred. Score 10; Mismatches

Similarity

52.6%;

No.

1.5e+03;

9;

Indels

0;

Gaps

DB 24; Length 24;

дb

IJ AAV45529/c

AAV45529 standard; DNA; 25 BP

AAV45529

15-FEB-1999

(first entry)

stomach cancer; ureG gene; PCR; primer;

W09844130-A1 Helicobacter pylori

Synthetic

Helicobacter pylori ureG gene PCR primer.

Vaccine; antigen; antigen; toxin; diagnosis; gastritis; ulcer;

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0;
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ABQ12221/c
                                                                                                                                                                            g
         Search completed: November 16, 2002, 02:15:58
                                                                                                                     Matches
                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ12221 standard; DNA; 25 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oligonucleotide adapter/capture probe 12212.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200216649-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2002
                                                                                                                                                                                                                     The invention relates to an oligonucleotide array (I) comprising at least 25 different addresses (adapter sequences) with each comprising a different capture probe selected from a group consisting of the sequences given in ABQ00010-ABQ13409. (I) is useful for immobilising a target nucleic acid sequence by attaching a dapter nucleic acid and contacting the modified target nucleic acid and contacting the modified target nucleic acid with (I). nucleic acid and contacting the modified target nucleic acid, The steps of above method is useful for detecting a target nucleic acid, which further comprises detecting the presence of the modified target middle target middle target middle target middle target middle target which further comprises detecting the presence of the modified target which further comprises detecting the presence of the modified target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-AUG-2001; 2001WO-US26519
                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 240; 261pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          different specific capture probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-292068/33.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-AUG-2000;
time : 260 secs
                                                                                                                                                                            Sequence 25 BP; 4 A; 5 C; 9 G; 7 T; 0 other;
                                                                                                                                                                                                             nucleic acid
                                                                                                                                     Local
                                                         24 CCAATATTACGTGACCACG 6
                                                                                      1 CCAATNUNNNNNNCCACG 19
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                                                                                                                                     Similarity
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                                                                                                                        Conservative
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31-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                    New chimeric proteins for use against Helicobacter pylori comprising an antigenic protein of H. pylori and Al and B subunits of Vibrio cholerae toxin, preferably produced by recombinant
                                                                                                                                                         pcR primers (see AAV45529 and AAV45530) are designed for the PCR amplification of the Helicobacter pylori ureg gene. The invention relates to recombinant DNA (see AAV62460-61) comprising a fusion gen prepared by ligating an antigenic determinant coding gene (e.g. the prepared by ligating an antigenic determinant coding gene (b.g. the ureg gene) of H. pylori and A2 and B subunit genes of Vibrio cholerae. Also claimed are chimeric proteins (see AAW80599-600) cholerae. Also claimed are chimeric proteins (see AAW80599-600) cholerae. Also claimed are chimeric production of the chimeric proteins, and use of the chimeric proteins in preventative and therapeutic vaccines for H. pyloriproteins in preventative and therapeutic vaccines for H. pyloriproteins diseases such as gastritis, gastric ulcer, duodenal associated diseases such as gastritis, gastric ulcer, duodenal
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Choi D,
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                                                                                                                 Sequence 25 BP; 7 A; 2 C; 8 G; 8 T; 0 other;
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20 CCAATTTTTACCATCCACG 2
                                                                         Local
                           1 CCAATNNNNNNNNCCACG 19
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   GenCore version Copyright (c) 1993 - 2002
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BE002165 PN2-BN0088
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BB197483 TC3-59E3.
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AV0710518 UR2-BT0268
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BG090373 mac19h08.
BF749006 MR2-BN038
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BF587741 BGCXNL5TR
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BH864991 SALK_0972
BF099257 CM4-UT004
AZ720239 RPCI-24-1
BH222899 1006109H0
AI938545 sb55b02 y
AW945325 PM3-EN000
BG950375 CM3-CT060
AG024826 Oryza sat
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BH223096 1006105C0
AA405167 ZU51h01. r
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Qy 1 Db 18 RESULT 2	Query Match Best Local Matches 1	BASE COUNT	COMMENT  FEATURES  Source	TITLE	ORGANISM REFERENCE AUTHORS	LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 BH857113	C C 88 C 88 C 88 C 88 C 88 C 88 C 88 C
CCAATUNUNUNUNUNCCACG	tch 52. al Similarity 52. 10; Conservative	/or//ob.//ob.//ob.//ob.//ob.//ob.//ob.//	Cont Sal) The 1001 Tel: Fax: Emai This TDNZ	A Sequence-Indexed Arabidopsis Genome Unpublished (2001)	Arabidopsis Eukaryota; V Spermatophyt Rosidae; eur 1 (bases 1 Alonso,J.M., .C., Jeske,A	BH857113 SALK_076821. Arabidopsis sequence. BH857113.1 GSS. thale cress.		10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 10 52.6 20 52.6
NCCACG 19        GCCACG 36	52.6%; score 10; DB 17; 52.6%; Pred. No. 1.5e+04; vative 0; Mismatches 9;	rgan.sm="Ar train="Colu b_xref="tax lone="SALK_ lone="ISALK_ lone="lob" a ote="por wa ch of which aments. The aments squ e site of found at	Ecker mnic Analysis Laborat for Biological Studi nes Road, La Jolla, C x1752 adu s sequence recovered e lies within an anno Dualifiers	Ecker, Library	tindiana iridiplantae; Streptophyta; iridiplantae; Streptophyta; a; Magnoliophyta; eudicotyje osids II; Brassicales; Brass to 43) Leisse T.J. Barajas, P., Ch Leisse M., Kim, C.J., Par)	43.44.95.x Arabidop thaliana genomic GI:21707434	ALIGNMENTS	173 12 BF748094 173 17 BH789270 174 9 AV004354 174 13 BJ121753 174 17 BH895513 175 9 AV022317 175 9 AA596238 175 17 BH855839 176 12 BF347368 178 9 A1937584 178 9 AV097435
	Length 43; ; Indels 0; Gaps 0;	mbia 0"  mbia 0"  076821.44.95.x"  076821.44.95.x"  rabidopsis thaliana TDNA insertion lines"  s performed on Arabidopsis thaliana lines  contains one or more TDNA insertion  resultant fragment for each line was  enced to determine the genomic sequence at  insertion. Details of the protocols used can  http://signal.salk.edu/tdna_protocols.html"  10 g 11 t	es A 92037, USA from the left border of tated exon of At4g29100.	Mutations in the	Embryophyta; Tracheophyta; dons; core eudicots; icaceae; Arabidopsis. en,H., Cheuk,R., Gadrinab er,H., Prednis,L., Shinn,P.	bp DNA linear GSS 08-JUL-2002 sis thaliana TDNA insertion lines clone SALK_076821.44.95.x, DNA		BF748094 MR2-BN038 BH789270 SALK_0014 AV004354 AV004354 BJ121753 BJ121753 BH895513 3526_1_34 AV022317 AV022317 AAS96238 vO30h10 r BH855839 SALK_0844 BF347368 602020556 AI937584 wp81c04.x AV097435 AV097435
RESULT 3 BQ756881 LOCUS DEFINITION	Qy 1 0	BASE COUNT ORIGIN Query Match Best Local Matches 1		FEATURES source		TITLE JOURNAL COMMENT	REFERENCE AUTHORS	AA475936 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
BQ756881 79 bp mRNA linear EST 26-JUL-2002 EBem09_SQ005_E15_R embryo, 1 Day germination, no treatment, cv Optic, EBem09 Hordeum vulgare cDNA clone EBem09_SQ005_E15 5', mRNA	CCAATNNNNNNNNCCACG 19         CCAATGGTTTAGCGCCACG 58	tch 19 a 10; Conssi	/strain="C57BL/GJ" /db_xref="taxon:10090" /clone="IMAGE:876475" /clone_lib="Soares_mammary_gland_NbMMG" /sex="male" /tissue_type="mammary gland" /dev_stage="4 weeks" /lab_host="DH10B" /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'			The WashU-HHMI Mouse EST Project Unpublished (1996) Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810	<pre>mammalla; wotherla; kodentla; sclurognath1; muridae; murinae; mus. 1 (bases 1 to 76) 1 (bases 1 to 76) Marra_M., Hillier_L., Allen_M., Bowles_M., Dietrich_N., Dubuque,T., Geisel_S., Kucaba_T., Lacy_M., Le,M., Martin_J., Morris_M., Schellenberg_K., Steptoe_M., Tan_F., Underwood_K., Moore_B., Theising_B., Wylie,T., Lennon,G., Soares_B., Wilson_R. and Waterston_R.</pre>	AA475936  ABELIANT OF TRIBUTED TO TR

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FEATURES
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                                                                                                                  TITLE
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genome Dynamics/Computational Biology Scottish Crop Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                        SALK_011672 Arabidopsis thaliana TDNA insertion lines thaliana genomic clone SALK_011672, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Waugh R, Marshall DF
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Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
                                                                Arabidopsis Genome
Unpublished (2001)
                                                                                                             Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Ga,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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00 44 1382 562426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"Vector: psporT1; Site_1: Sal I; Site_2: Not I; Non-normalised library, directionally cloned into psporT1. Derived from embryos dissected from germinating grains (1 day) in glasshouse grown barley plants. Developed as part of the barley transcriptome resources of BBSRC/SEERAD funded cereal IGF (Investigating Gene Function) project."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="embryo"
/dev_stage="1 Day germination"
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Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ph28h02.y2 Ostertagia ostertagi L3 pAMP1 v1 Ostertagia ostertagi cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Class: TDNA tagged
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                                                                                                                                                                                              at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center High quality sequence stop: 69.
                                                                                                                                                                                                                                                                                                                                                                         The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, K., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J., Wylie,T.,
    Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Washington Univ. Nematode EST Project, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ099298.1 GI:20132282
                                                                                                                                                                                                                                                                          The library was constructed by Claire Murphy and Dr. James McCarter
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: McCarter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichostrongyloidea; Haemonchidae; Ostertagiinae; Ostertagia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ostertagia ostertagi.
                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" a 20 c 21 g 19 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PCR was performed on Arabidopsis thaliana lines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="SALK_011672"
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                       /clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
/dev_stage="L3"
/lab_host="DH10B"
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                                                                                               /organism="Ostertagia ostertagi"
/db_xref="taxon:6317"
/note="Vector: pAMP1 (Gibco); Site_1: NotI; Site_2: SalI;
                                                                                                                                                                      Location/Qualifiers
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Pred. No. 1.9e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence submitted separately Plate: 1006166 row: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible ligation site so sequence was trimmed. Post-ligation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stanford University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize genomic sequences found using engineered RescueMu transposon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               walbot@stanford.edu
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units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA v
                                                                        /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BanHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           larvae were collected from 14 day fecal-sphagnum moss cultures of Ostertagia eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                          /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
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                                                                                                                                                                                                                                              /tissue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                     /lab_host="DH10B"
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Zea mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Very probable ligation site found so sequence was trimmed. Post-ligation sequence submitted separately. Plate: 1006105 row: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Class: transposon-tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stanford University
855 California Ave, Palo Alto, CA 94304, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department of Biological Sciences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Walbot V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maize genomic sequences found using engineered RescueMu transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walbot, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: walbot@stanford.edu
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      Conservative
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                                                                                                                                                       note="organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BgIII, and ligated to form circular plasmids DH10B
                                                                                                                        cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="leaf"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                            /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="1006 - RescueMu Grid G"
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LOCUS BF086094 100 bp mRNA linear EST 19-OCT-200 DEFINITION CM3-GN0052-080900-334-c11 GN0052 Homo sapiens cDNA, mRNA sequence
                                                                               RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peterson, D.G., Schulze, S.R., Sciara, E.B., Lee, S.A., Bowers, J.E., Nagel, A., Jiang, N., Tibbitts, D.C., Wessler, S.R. and Paterson, A.H. Integration of Cot analysis, DNA cloning, and high-throughput sequencing facilitates genome characterization and gene discovery denome Res. 12 (5), 795-807 (2002)
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Room 162, Riverbend Research Bldg., 110 Riverbend Rd., Athens, GA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"vector: pGEM-TA-Easy: A Cot analysis was performed /note-"vector: pGEM-TA-Easy: A Cot analysis was performed for the sorthum genome. Based on the resulting Cot curve, bydroxyapatite chromatography was used to isolate chipy repetitive (MR), 'moderately-repetitive (MR), 'moderately-repetitive (MR), and 'single/low-copy' (SL) sequence components from the collinor based DNA sheared genomic DNA. The three repetition based DNA components were cloned into E. coll to produce HRCot, and SLCot genomic libraries. Blotting and MRCot, and SLCot genomic libraries. Blotting and sequencing data indicates that each library is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 representative of the component from which it was derived. putative ID listings given for sequences are based on comparison (blastn) with sequences in the NCBI NI Database. Only the primary match is given (all primary E values are < or = 1.00E-5). In no instance does a 'Cot values are < or = 1.00E-5).
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence start: 5 High quality sequence stop: 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM3-GN0052-080
900-334-c11&t3=2000-09-08&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL
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                                                                                                                                                                                                                                                                                                                                                                                      BOGXN16TR BOGX Brassica oleracea genomic clone BOGXN16, DNA
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1 (bases 1 to 101) Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M
                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning; products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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52.6%;
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Pred. No. 2.1e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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OM23D01:S1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
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Fax: 301-838-0208
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/note=Torgan: pooled: Vector: pTTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized NII raries (fetal lung whili9W, testis NHT, and B-cell Vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made in the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239,
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/clone="IMAGE:1541833"
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/strain="T01000H3"
/db_xref="taxon:3712"
/clone="BOGXN16"
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BF094257 110 bp mrNA linear EST 19-OCT-200CM4-UT0042-050900-568-ell UT0042 Homo sapiens cDNA, mrNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: TDNA tagged
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 109)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                 directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can
                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="SALK_097225"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="Columbia
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52.6%;
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52.6%;
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Pred. No. 2
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24 g
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                                                                                                                                                                                                    Mismatches
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                      EST 19-OCT-2000
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CCAATNUNNNNNNCCACG 19
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1 (bases 1 to 110)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                      AZ720239
AZ720239.1 GI:12461733
                                                                                                                                                                                                                                                   AZ720239 110 bp DNA linear GSS 24-JAN-200 RPCI-24-104K1.TV RPCI-24 Mus musculus genomic clone RPCI-24-104K1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=at2=CM4-UT0042-050
900-568-e11&t3=2000_09-05&t4=1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                Mammalia; Eutheria; Rodentia; 1 (bases 1 to 110)
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                  Mus musculus
                                                                                                                                                                   GSS
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Fax: +55-11-2707001
    Tsegaye,G.,
                                                                                                                                                                                                                                       DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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BF094257.1 GI:10899967
                                                                                                                                           house mouse
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                     Nierman, W.,
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38 c 23 g 23 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone_lib="UT0042"
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    Geer, K.,
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52.6%;
  Krol, M.,
                     Malek,J.,
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Pred. No. 2.2e
0; Mismatches
Shvartsbeyn, A.,
                        Shatsman, S., Akinret, B.,
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GSS.
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10; Conserv
Class: transposon-tagged
                   Email: walbot@stanford.edu
Possible ligation site so sequence
sequence submitted separately.
Plate: 1006109 row: 15
                                                                                           Tel: 650 723 2227 Fax: 650 725 8221
                                                                                                                            855 California Ave,
                                                                                                                                                  Stanford University
                                                                                                                                                                 Department of Biological Sciences
                                                                                                                                                                                       Contact: Walbot V
                                                                                                                                                                                                        Unpublished (2001
                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                         Zea mays
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Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other_GSSs: RPCI-24-104K1.TJ
                                                                                                                                                                                                                          Maize genomic sequences found using
                                                                                                                                                                                                                                               Walbot, V.
                                                                                                                                                                                                                                                                                                                                                            Zea mays.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/orderingframe.htm). i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shaying Zhao
                                                                                                                                                                                                                                                               (bases 1 to 113)
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
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/strain="C57BL/6J"
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/clone="RPCI-24-104K1"
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                                                                                                                              Palo Alto,
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Pred. No. 2.2e+04;
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                                                      was trimmed. Post-ligation
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sb55b02.y1 Gm-c1018 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-c1018-4 5' similar to TR:Q38910 Q38910 XYLOGLUCAN
ENDOTRANSGLYCOSYLASE-RELATED PROTEIN. ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
                                                                                                                                                                                                                                                                                                                                       Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C. Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schur, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.
                                                                                                                                                Possible reversed clone: similarity on wrong strand This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800
                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycine max
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                                                                            High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                    Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                               Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                              Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                  est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pBlueScript backbone); Site_1: BamHI; Site_2: BgIII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BgJII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ampicillin.
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/db_xref="taxon:4577"
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/organism="Glycine max"
                                                 Location/Qualifiers
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Pred. No. 2.2e+04;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dias Neto, E., García Correa, R., Verjovski-Almeida, S., Briones, M.R., Ragai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence tags
                                                                                                                                                                              400-001-g04&t3=2000-04-28&t4=1)
                                                                                                                                                                                                                               Project.
                                                                                                                                                                                                                                                                                                                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20202663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                   Seq primer: puc 18 forward
                                                                                                                                                                                                       Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM3-EN0004-280
                                                                                                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome
                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases
                                                                                               quality sequence start: 20 quality sequence stop: 114.
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                                                                                                                                                                                                                                                                                                                                       +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr. John Erpelding."

3 C 25 g 24 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript II XR: Site_1: EcoRI; Site_2: XhoI; This cDNA library was constructed from mRNA isolated from 2-3 week old greenhouse grown plants. The cDNA library was prepared using the Stratagene pBluescript II XR library construction kit. Complementary DNA was synthesized from mRNA using a primer consisting of a poly (dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1018-4"
/clone_lib="Gm-c1018"
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/dev_stage="2-3 weeks old"
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/db_xref="taxon:9606"
                        /organism="Homo sapiens"
                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.bb/Scripts/gethtml2.pl?tl=CM3&t2=CM3-CT0603-040101-611-h01&t3=2001-01-04&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/dev_stage="Adult"
                /note="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196.,716. Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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URL:http://tos.nias.affrc.go.jp/, Tel:81-298-38-7020,
Fax:81-298-38-7020)
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Miyao,A., Miyazaki,A., Yamashita,Y. and Hirochika,H.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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UI-R-C3-tu-f-02-0-UI.sl UI-R-C3 Rattus norvegicus cDNA clone
UI-R-C3-tu-f-02-0-UI 3', mRNA sequence.
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                                                               sequence.
BH230343
                                                                                                      \tt BH230343 120 bp DNA linear GSS 08 1006157D12.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                        BH230343.1 GI:16833394
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The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail.cDNA Library Preparation: M.B. Soares Lab Clone distribution:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: M13 Forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein Medical Research Building Towa City, IA 52242, USA Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 119)
Bonaldo, M.F., Lenno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        library (UIR-C3) was constructed as follows: PCRamplified cDNA inserts from UIR-C2p clones from which 3' ESTs had been derived was used as a driver in a hybridization with the UIR-C2p library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (LifeTechnologies) to generate the UIR-C3 library. This procedure has been previously described (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kidney, heart, spleen, ovary, muscle, and 8, 12 and 18 day embryos, after a series of subtractions to reduce the representation of cDNAs from which ESTs had already been generated. The following serially subtracted libraries were generated in this process: UI-R-C3, UI-R-C2p, UI-R-C1, UI-R-C0, UI-R-A1, UI-R-E1. The tag is a string of 3.5 nucleotides present between the Not I site and the oligo-dT track whichallows identification of the library of origin of a clone within themixture. The subtracted itherery of origin of a clone within themixture. The subtracted
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/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C3 library is a subtracted library of a series, ultimately derived from a mixture of individually tagged normalized derived from raf placenta, adult lung, brain, included the control of the contr
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/db_xref="taxon:10116"
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                     Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001) Contact: Walbot V
Department of Biological Sciences
                                                                                                                                   Walbot, V
                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
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pBlueScript backbone); Site_1: BamHI; Site_2: BglII;
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855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , O.T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zu51h01.rl Soares ovary tumor NoHOT Homo sapiens cDNA clone
IMAGE:741553 5', mRNA sequence.
                                                                                                                                                                                                                                                                        Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck,EST_Project 1997
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                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1, (bases 1 to 123)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                      Unpublished (1997)
                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                     Contact: Wilson RK
                                                          IMAGE Consortium (info@image.linl.gov) fo
Seq primer: -28m13 rev2 ET from Amersham
                                                                                                 This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         650 725 8221
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was 'RescueMu.' and lasf punches, double digested using BamHI extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B and By were transformed and then screened on LB plates with
                                                                                                                               est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; pBlueScript backbone); Modified maize Mu transposon RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
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/dev_stage="adult"
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/organism="Homo sapiens"
                                       Location/Qualifiers
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52.6%;
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Pred. No. 2.3e+04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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ORIGIN
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                                                                                                                                                                                                                                                                                                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insertion site preferences of the P transposable element in {\tt Drosophila} melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3347-3351 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AQ073902.1 GI:3403944
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University of California, Berkeley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Gerald Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20202638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The P element insertion position is base 117 in the 124 bases. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence orientation is forward strand relative to 5' end of P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 5106439947
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                                                                                                                                                                                                                                                                                                                                                                               Class: transposon-tagged
                                                                                                                                                                                                                                                                                                                                                                                                                    recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 insertion position refers to the first base of the 8 base target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gerry@fruitfly.berkeley.edu
ce recovery method was inverse PCR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="ovarian tumor"
/tissue_type="ovarian tumor"
/lab_host="DH10B (ampicillin resistant)"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: ovary 'vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st modified polylinker; Site_1: Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (strand cDNA was primed with a Not I - oligo(dT) primer (stra
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/clone="IMAGE:741553"
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37 c 27 g
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                            /clone_lib="Drosophila melanogaster EP line"
/note="Inverse PCR was performed on Drosophila ingle EP
melanogaster strains each of which contains a single EP
transposable element insertion. (The generation of these
transposable element insertion for the performed of these
insertion strains is described in Rorth P, Szabo K, Bailey
A, Laverty T, Rehm J, Rubin GM, Weigmann K, Milan M, Benes
                                                                                                                                                                                                                                                                 /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                /db_xref="taxon:7227"
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Pred. No. 2.3e+04;
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BH812753/c
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                                                                                                                              Query Match
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                                                                                                        Similarity
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn, Zimmerman,J. and Ecker,J.R.
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SALK_063023 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_063023, DNA sequence.
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                                                                                                                                                                     /note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html" a 13 c 39 g 43 t
                                                                                                                                                                                                                                                                                                                      /clone_lib="Arabidopsis thaliana TDNA insertion lines"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/strain="Columbia 0"
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                                                                                                   52.6%;
52.6%;
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                                                                                            Score 10; DB 17; Length 124; Pred. No. 2.3e+04;
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Maize genomic sequences found using engineered RescueMu transposon
                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoldeae; Andropogoneae; Zea.
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AZ919927
AZ919927.1 GI:13390126
                                       Walbot, V
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The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
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A Sequence-Indexed Library of Insertion Mutations in the
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids.II; Brassicales; Brassicaceae; Arabidopsis.
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/note="pCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

30 c 35 g 31 t
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RESULT 28
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                                                                                                     Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA
Tel: 650 723 227
Fax: 650 725 8221
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Class: transposon-tagged
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                    Reverse complemented post-ligation sequence from source sequence Plate: 3526_1_35_1 row: 27
                                                                                                                                                                                                                 Contact: Walbot V
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                                                        Possible ligation site of ends cut by 2 different endonucleases
                                                                                 Email: walbot@stanford.edu
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Contact: Walbot V
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/db_xref="taxon:4577"
/clone_lib="1006 - RescueMu Grid G"
/tissue_rype="leaf"
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2.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: +55-11-2704922
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Ludwig Institute for Cancer Research
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/db_xref="taxon:9606"
                            /organism="Homo sapiens"
                                                                                                        Location/Qualifiers
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/dev_stage="adult"
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/cultivar="mixed background w23/A188/B73"
/db_xref="taxon:4577"
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Pred. No. 2.3e+04;
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                                                                                                                                                                                                                                                                                                                                                                                 Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVZ&t2=QV2-NN0042-
210800-310-d07&t3=2000-08-21&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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Shotgun sequencing of the human transcriptome with ORF expressed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: +55-11-2704922
Fax: +55-11-2707001
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/dev_stage="Adult"
                 /note="organ: nervous_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                  /clone_lib="NN0042"
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/db_xref="taxon:9606"
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Search completed: November 16, 2002, 03:32:34 Job time: 1980 secs
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                                                                                                     Conservative
                                                                                                                 52.6%;
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Pred. No. 2.4e+04;
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Perfect score:
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  No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

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149.377 Million cell updates/sec
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Match Length
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   Gapext 1.0
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US-09-86-373-1152

US-09-867-701-3962

US-09-974-300-8096

US-09-978-320-59

US-09-910-689-59

US-09-910-742-59

US-09-783-550-10136

US-09-77-564-1013

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US-10-007-805-206

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US-10-007-805-206

US-10-007-805-206

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 Sequence 35, Appl
Sequence 3962, Ap
Sequence 3962, Ap
Sequence 8096, Ap
Sequence 59, Appl
Sequence 59, Appl
Sequence 10136, A
Sequence 1013, Ap
Sequence 1185, A
Sequence 206, App
Sequence 206, App
Sequence 1836, Ap
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                                                Sequence 246, App Sequence 6179, Ap Sequence 1180, Ap Sequence 1171, App Sequence 1451, App Sequence 1451, App Sequence 2907, App Sequence 1113, Ap Sequence 1113, Ap Sequence 1144, Ap Sequence 1148, Ap Sequence 1484, Ap Sequence 1485, App Sequence 350, App Sequence 4036, Ap Sequence 4036, Ap Sequence 4115, Ap Sequence 41174, App Sequence 41174, App Sequence 1592, Ap Sequence 1592, Ap Sequence 1592, Ap Sequence 1592, Ap Sequence 11304, Mp Sequence 1130, App Sequence 1140, Ap Sequence 1518, App Sequence 518, App Sequence 518, App Sequence 1518, App Sequence 518, App Sequence 518, App Sequence 518, App Sequence 1518, App Sequence 1518, App Sequence 1518, App Sequence 1518, App Sequence 518, App Sequence 519, App Sequence 510, App Sequence 510, App Sequence 510, App Sequence 510, App Sequence 310, App Sequence 510, App Sequence 310, 
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                              8472,
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Result

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ALIGNMENTS

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; Sequence 1152, Application US/09969373

; Patent No. US20020133852A1
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                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Effertz, Roger J.
APPLICANT: Hauge, Brian M.
TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
FILE REFERENCE: 38-10(52679)A
CURRENT APPLICATION NUMBER: US/09/969,373
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: US 09/754,853
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
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                                                                                                                                                                                           SEQ ID NO 1152
LENGTH: 100
                                            Matches
                                                                                    Query Match
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Best Local Similarity
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LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Daewoong Pharmaceutical Co, LTD
APPLICANT: Kim, Byung-O
APPLICANT: Shin, Sung-Seup
APPLICANT: Yu, Young-Hyo
APPLICANT: Park, Myung-Hwan
APPLICANT: Choi, Deck-Joon
APPLICANT: Choi, Deck-Joon
APPLICANT: Jung, Hyung-In
TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Heliot
FILE REFERENCE: 0136/0G140
                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 09/855,768
PRIOR FILING DATE: 2001-05-15
NUMBER OF SEQ ID NOS: 4593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/402/100 CURRENT FILING DATE: 1999-09-27 EARLIER APPLICATION NUMBER: KR 97-11950 EARLIER FILING DATE: 1997-03-31 EARLIER APPLICATION NUMBER: KR 97-11951 EARLIER FILING DATE: 1997-03-31
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/760,427 PRIOR FILING DATE: 2001-01-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn version 3.0
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                                                                                                                                                                         TYPE: DNA
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NAME/KEY: misc_feature
LOCATION: ()..()
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1 CCAATNUNNNNNNCCACG 19
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52.6%;
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                                   Score 10; DB 10; L. Pred. No. 3.3e+02;
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Pred. No. 2.4e+02;
0; Mismatches 9;
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SEQ ID NO 8096
LENGTH: 210
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
                                                                                                                                                            Matches
                                                                                                                                                                                               Query Match
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APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-US
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SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(210)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                             ORGANISM: Bacillus clausii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 123
TYPE: DNA
                                                                         152 CCAATTTCGTCTGTCCACG 134
                                                                                                                                                        Local Similarity nes 10; Conserv
                                                                                                                 1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CCAATNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCAATCATTTCCATCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 4.0
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                        52.6%;
52.6%;
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52.6%;
                                                                                                                                                        0;
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                                                                                                                                                                        Score 10; DB 10;
Pred. No. 3.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 10; DB 10; pred. No. 3.4e+02; 0; Mismatches 9;
                                                                                                                                                        Mismatches
                                                                                                                                                                                         Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 123;
                                                                                                                                                      0,
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                                                                                                                                                    Gaps
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                                                                                                                                                    0,
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APPLICANT:
APPLICANT:

GENERAL INFORMATION:

Sequence 59, patent No. U

9, Application US/09778320 US20010034052A1

APPLICANT:
APPLICANT:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature; LOCATION: 34, 120, 153, 159, 171, 179, 184, 194, 197; OTHER INFORMATION: n = A,T,C or G US-10-010-742-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. US20020146727A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-783-590-10136
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Dillon, Day Applicant: Day, Craig H.
                                                                                                                                                                                                                                                                                                                                                                 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/010,742
CURRENT FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER FILE REFERENCE: 210121.491C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10136, Application US/09783590 Patent No. US20020110850A1
                                                                                                                                                                                                                                                                                                                 APPLICANT: Dillon, Patrick J.
APPLICANT: Haseltine, William A.
APPLICANT: Li, Hacoong
                                                                                                         SOFTWARE: PatentIn Ver. SEQ ID NO 10136
                                                                                                                                                                                                                                                    APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                      PRIOR APPLICATION NUMBER: 08/420,856
PRIOR EILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
NUMBER OF SEQ ID NOS: 12485
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/783,590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                       CURRENT FILING DATE:
OTHER INFORMATION: n equals a,t,g, or c
                                                              ORGANISM: Homo sapiens
                                                                             TYPE: DNA
                               NAME/KEY: misc feature
                                                FEATURE:
                                                                                              LENGTH:
                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88 CCAATTCTTCATCTCCACG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAATNUNNNNNNNCCACG 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214
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                                                                                                219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houghton, Raymond L. Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bennington, Angela
Zehentner, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang, Tongtong
McNeill, Patricia D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jiang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fanger, Gary R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Davin C.
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                                                                                                                                                                                                                                2000-02-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 10; DB 12;
Pred. No. 3.9e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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0

NAME/KEY: misc\_feature
LOCATION: (1)...(214)
OTHER INFORMATION: n = A,T,C or G
US-09-778-320-59

SEQ ID NO 59 LENGTH: 214

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

SOFTWARE:

CURRENT APPLICATION NUMBER: US/09/778,320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301

FastSEQ for Windows Version 3.0

TITLE OF INVENTION:

FILE REFERENCE:

210121.491C5

DIAGNOSIS OF BREAST CANCER

COMPOSITIONS AND METHODS FOR THE THERAPY AND

APPLICANT: APPLICANT:

Mang, TongTong
McNeill, Patricia D.

Houghton, Raymond L. Mitcham, Jennifer Jiang, Yuqıu Day, Craig H. Dillon, Davin C.

QΥ

Matches Query Match

10;

Conservative

0; Mismatches score 10; DB 10; pred. No. 3.9e+02;

DB 10;

Length 214;

Indels

0

Gaps

Local

Similarity

52.6%;

US-09-910-689-59/c

Sequence 59, Application US/09910689 Patent No. US20020081609A1

GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yuqiu

APPLICANT:
APPLICANT:

APPLICANT:

Wang, Tongtong McNeill, Patricia D. Houghton, Raymond Mitcham, Jennifer

Raymond L.

APPLICANT:

US-09-910-689-59

ORGANISM: Homo sapiens

TYPE: DNA ENGTH: 214

Query Match

h 52.6%; Similarity 52.6%;

Score 10; DB 10; Pred. No. 3.9e+02; Mismatches

9; Indels Length 214;

0;

DB 10;

ocal

Matches

10;

Conservative

SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 59

APPLICANT: HATLOCKEY, SUSAN L.
APPLICANT: HATLOCKEY, SUSAN L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIACNOSIS OF BREAST CANCER FILE REFERENCE: 210121.491C6
CURRENT FILLING DATE: 2001-07-20
CURRENT FILLING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307

Вþ QY

OTHER INFORMATION: n equals a,t,g, or

NAME/KEY: misc feature

LOCATION:

NAME/KEY: misc feature

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SOFTWARE: FastSEQ for Wi
SEQ ID NO 1013
LENGTH: 237
TYPE: DNA
ORGANISM: Homo sapiens
US-09-777-564-1013
         DЬ
                                     Qy
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                                                                         Query Match
Best Local Similarity
                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             Sequence 1013, Application US/09777564
Patent No. US20020022591A1
                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
                                                                                                                                                                                                                                              TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REPERENCE: 210121.493
                                                                                                                                                                                                                                                                                                APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: n equals a,t,g, or c
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18 CCAATTTCAGCCTGCCACG 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature LOCATION: (186)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: n equals a,t,g, or c
                           1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature LOCATION: (182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: n equals a,t,g, or c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CCAATNUNNNNNNNCCACG 19
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                                                               10;
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                                                                                                                                                                                      FastSEQ for Window Version 4.0
                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (36)
                                                                 52.6%; Score 10; DB 10;
52.6%; Pred. No. 4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52.6%;
                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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Pred. No. 3.9e+02;
Pred. No. 3.9e+02;
                                                                               DB 10; Length 237;
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                                                  9;
                                                  Indels
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                                             0,
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; APPLICANT: Jiang, Yuqiu
; APPLICANT: Dillon, Davj
                                                                                            Sequence 206, Application US/09604287A Patent No. US20020064872A1
                                                                                   ; GENERAL INFORMATION:
                                                                                                                                 US-09-604-287A-206
                                                                                                                                                    RESULT 12
                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                             US-09-878-574-6181
      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thomson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TILE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILLING DATE: 2001-12-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-878-574-6181/c
                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 6181
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 56-LIB34-004-Q1-E1-F8
US-09-960-352-13155
                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 13155
LENGTH: 238
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-960-352-13155/c

Sequence 13155, Application US/09960352

Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6181, Application US/09878574 Patent No. US20020110548A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: 701097950H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: WUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION UNMERS: US/09/960,352
NUMBER OF SEC TO NOTE: 2001-09-24
NUMBER OF SEC TO NOTE: 2001-09-24
NUMBER OF SEC TO NOTE: 2001-09-24
                                                                                                                                                                                            242 CCAATAACTGTTCGCCACG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APFLICANT: Warren,
                                                                                                                                                                                                                          1 CCAATNUNNNNNNNCCACG 19
                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 CCAATATGTTAGATCCACG 141
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les 10; Conserv
                                                                                                                                                                                                                                                                  10;
Xu, Jiangchun
Harlocker, Susan L.
                               Mitcham, Jennifer L.
                                             Dillon, Davin C
                                                                                                                                                                                                                                                             Conservative
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Byatt, John C
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                                                                                                                                                                                                                                                                          52.6%;
52.6%;
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52.6%;
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                                                                                                                                                                                                                                                                       Score 10;
Pred. No.
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Pred. No. 4e+02;
                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                     4e+02;
                                                                                                                                                                                                                                                                                DB 10; Length 247;
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                                                                                                                                                                                                                                                9; Indels
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                                                                                                                                                                                                                                           Gaps
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-604-287A-206
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US-09-339-338-206
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 206
LENGTH: 261
                                                                                                                                                                                                                                                                                                          RESULT 14
US-10-007-805-206
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CURRENT APPLICATION NUMBER: US/09/604,287A
CURRENT FILING DATE: 2000-06-22
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yuqiu, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIANOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C2
                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                         Sequence 206,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 315
                                                                                         APPLICANT:
APPLICANT: Durham, Margarita
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C10
                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                     APPLICANT: Jiang, Yuqiu
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                                                                          APPLICANT:
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                                                                                                                                                                                                                                                                          06, Application US/10007805
US20020150581A1
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                                                                        Fanger, Gary R. Vedvick, Thomas S. McNeill, Patricia D.
                                                                                                                                               Harlocker, Susan L.
Hepler, William T.
                                                                                                                                                                                   Xu,
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                                                                                                                              Henderson, Robert A.
                                                                                                                                                                                                       Mitcham, Jennifer L.
                                                                                                                                                                                                                        Dillon, Davin C
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52.6%; Pred. No. 4e+02;
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Pred. No. 4e+02;
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APPLICANT: Xu, Jiangchun
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.547c1
CURRENT APPLICATION NUMBER: US/10/033,528
CURRENT FILING DATE: 2001-12-26
NUMBER OF SEO ID NOS: 1896
SOFTWARE: FastSEQ for Windows Version 4.0
SEO ID NO 1836
LENGTH: 262
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Patent No. US20020131971A1
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CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 593
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                sequence 1896, Application US/09294093B
patent No. US20010051335A1
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                                                                                                              SEQ ID NO 1896
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                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 199-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
                                                                                                                                                                                                                                    APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL FILE REFERENCE: PL-0009 US
                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                SOFTWARE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20010051335A1 700345158H1
                                                         ORGANISM: Zea mays
                                                                        TYPE: DNA
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                                   FEATURE:
                                                                                          LENGTH: 267
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                                                                                                                                  PERL Program
                                                                                                                                                                                                                                                                                                                 Lalgudi, Raghunath, V.
                                                                                                                                                     April 21, 1909
38:
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Pred. No. 4e+02;
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Pred. No. 4.1e+02;
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RESULT 18
US-09-783-590-11139/c
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                                                    PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
PRIOR FILING DATE: 1994-11-21
                                                                                                             CURRENT APPLICATION NUMBER: US/09/783,590 CURRENT FILING DATE: 2000-02-15 PRIOR APPLICATION NUMBER: 08/420,856
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                             SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                             APPLICANT: Rosen, Craig A.
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
FILE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                     APPLICANT: Dillon, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 5857
LENGTH: 268
                                                  NUMBER OF SEQ ID NOS: 12485
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APPLICANT: Sherman, Bradley K.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN SEEDLING
FILE REFERENCE: PL-0012-1 CON
CURRENT APPLICATION NUMBER: US/09/923,876
CURRENT FILING DATE: 2001-08-06
CURRENT FILING DATE: 2001-08-06
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NUMBER OF SEQ ID NOS: 6332
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PRIOR APPLICATION NUMBER: 60/085,331
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PRIOR FILING DATE: 1999-04-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Incyte ID No. US20020013958A1 700457860H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: 65, 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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LOCATION: 8, 24, 45, 69, 106, 174, 192, 197, 199-200, 206-207, 209, 227, 257,
OTHER INFORMATION: a, t, c, g, or other
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                                                                                                                                                                                                                                                                                                         INFORMATION:
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                                                                                                                                                                                                                                                    Li, Haodong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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52.6%;
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57.9%;
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Pred. No. 4.1e+02;
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Pred. No. 4.1e+02;
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                                                                                    ; ORGANISM: Homo sapien US-09-867-701-5278
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-867-701-5278/c
                                                                                                                                      SEQ ID NO 5278
LENGTH: 274
   Best Local Similarity 52.6%;
Matches 10; Conservation
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           Sequence 5278, Application US/09867701 Patent No. US20020132237A1
                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FRASSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                 APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                      APPLICANT: Aglate, Paul A. APPLICANT: Jones, Robert
                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 11139
LENGTH: 271
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LOCATION: (259)
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57.9%;
 Score 10; DB 10; Pred. No. 4.1e+02; No. Mismatches 9;
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Pred. No.
                                   DB 10; Length 274;
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Gaps
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; OTHER INFORMATION: Clone ID: LIB3028-053-Q1-B1-D5
US-09-878-574-246
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US-09-878-574-246
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SEQ ID NO 3259
LENGTH: 283
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Patent No. US20010051335A1
GENERAL INFORMATION:
                                                                        Matches
                                                                                           Best
                                                                                                            Query Match
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SEQ ID NO 246
LENGTH: 280
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                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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FILE REFERENCE: 38 2-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
                                                                                                                                                     NAME/KEY: unsure
LOCATION: 33, 53
OTHER INFORMATION: a, t, c, g, or other
                                                                                                                                                                                                          NAME/KEY: misc_feature OTHER INFORMATION: Incyte ID No. US20010051335A1 700379672H1
                                                                                                                                                                                                                                                                      ORGANISM: Zea mays
                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                         Local Similarity
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                                 1 CCAATNUNNNNNNNCCACG 19
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CCAATCCCCTTTCCCCACG 22
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                                                                       Conservative
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52.6%;
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52.6%;
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                                                                                  Score 10; DB 10;
Pred. No. 4.1e+02;
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Pred. No.
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                                                                     Mismatches
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                                                                                                     Length 283;
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                                                                   Indels
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SEQ ID NO 6179
LENGTH: 293
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                                                                                                                                                                                                                         SEQ ID NO 8100
LENGTH: 306
TYPE: DNA
ORGANISM: Bacillus clausii
                                             Matches
                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500.US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILLING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER: GEO. TO. NUMBER: 60/279,526
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Patent No. US20010051335A1
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYNUCLEOT
FILE REFERENCE: PL-0009 US
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                                                                                                                                         NAME/KEY: misc_feature
LOCATION: (1)...(306)
OTHER INFORMATION: n = A,T,C or
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NAME/KEY: unsure
LOCATION: 250, 255-256
OTHER INFORMATION: a, t, c, g, or other
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                            Match 52.6%;
Local Similarity 52.6%;
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1 CCAATNUNNNNNNNCCACG 19
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                                           10;
                                      Conservative
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52.6%;
                                Score 10; DB 10; Le
Pred. No. 4.2e+02;
Pred. No. 4.2e+02;
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94 CCAATTTCGTCTGTCCACG 112

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RESULT 24
US-09-878-574-1186/c
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US-09-938-842A-1451/c
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                                                                       Db
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US-09-728-444-594/c
              RESULT 26
                                                                                                                                                                                                                                                                    SEQ ID NO 1451
LENGTH: 351
TYPE: DNA
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CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 1186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1451, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(15401)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Byrum,
APPLICANT: La Ro:
APPLICANT: Thomp:
                                                                                                                                                     Matches
                                                                                                                                                                          Best
                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE FILE REFERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Harper, Jeff APPLICANT: Kreps, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Xun APPLICANT: Zhu, Tong
                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Glycine max
OTHER INFORMATION: Clone ID: LIB3028-041-Q1-B1-A12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 339
                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   164 CCAATGAATGTAAACCACG 146
                                                                         143 CCAATCAGAGCCTGCCACG 125
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les 10; Conserv
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                                                                                                              1 CCAATNUNNNNNNCCACG 19
                                                                                                                                                                      Local Similarity
                                                                                                                                                     10;
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Thompson, Michael D.
                                                                                                                                                   Conservative
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                                                                                                                                                   52.6%; Score 10; DB 9; Le
52.6%; Pred. No. 4.3e+02;
... Mismatches 9;
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52.6%;
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Pred. No. 4.3e+02;
0; Mismatches 9
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                                                                                                                                                                                          Length 351;
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; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(358)
; OTHER INFORMATION: n = A,T,C or
US-09-728-444-594
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; ORGANISM: Arabidopsis thaliana US-09-770-791-478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 594
LENGTH: 358
TYPE: DNA
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                                                                         NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 478
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APPLICANT:
APPLICANT:
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APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. US20020161207A1el Murine Polynucleotide Sequences
TITLE OF INVENTION: and Mutant Cells and Mutant Animals Defined Thereby
FILE REFERENCE: LEX-0100-USA US/09/728,444
CURRENT APPLICATION NUMBER: US/09/728,444
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR APPLICATION NUMBER: US 60/168,360
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 1206
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                 TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thaliana
FILE REFERENCE: 2029 (PARA-018PRV)
CURRENT FILLING NUMBER: US/09/770,791
CURRENT FILLING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,480
PRIOR APPLICATION NUMBER: 60/178,480
                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                     PRIOR FILING DATE:
                                                                                                                                                                                                                                                                            APPLICANT:
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                                                       LENGTH: 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Tambaka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An, Yong-Qiang
Hamilton, Carol M.
                                                                                                                                                                                                                                                                          Hurban, Patrick
                                                                                                                                                                                                                                                                                                               Davis, Keith R. Allen, Keith
                                                                                                                                                                                                                                                                                                                                                                                                             Woessner, Jeffrey P. Haas, William David
                                                                                                                                                                                                                                                                                          Hoffman, Neil
                                                                                                                                                                                                                                                                                                                                                    Slader,
                                                                                                                                                                                                                                                                                                                                                                      Kricker, Maja
                                                                                                                                                                                                                                                                                                                                                                                         Garcia, Carlos A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matthew,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Raines,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Price, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abraham V.
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52.6%;
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Pred. No. 4.3e+02;
Pred. No. 4.3e+09; Indels
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                                                                                                                ; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORWATION: Clone ID: LIB3028-018-Q1-B1-D9
US-09-878-574-2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:

NAME/KEY: misc_feature

: LOCATION: (1)...(365)

: OTHER INFORMATION: n = A,T,C or G

US-09-563-817-177
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US-09-563-817-177
; Sequence 177, Application US/09563817
; Patent No. US20020095031A1
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                                                                                                                                                                 APPLICANT: Byrun, Joseph R. J.
APPLICANT: Hompson, Michael D.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(15401)
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-06-14
NUMBER OF SEQ ID NOS: 15775
SEQ ID NO 2907
LENGTH: 367
                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/563,817
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: US 60/132,343
PRIOR FILING DATE: 1999-05-04
NUMBER OF SEQ ID NOS: 1008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 177
                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2907, Application US/09878574 Patent No. US20020110548A1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Nehls, michael C.
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. US20020095031A1el Human Polynucleotides and the TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: LEX-0021-USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 CCAATTCTGTCATTCCACG 262
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1 CCAATNUNNNNNNNCCACG 19
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                                       10;
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                                       Conservative
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52.6%;
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                                     0,
                             Score 10; DB 10, Pred. No. 4.4e+02; ""matches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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Pred. No. 4.4e+02;
0; Mismatches 9;
                                                                  DB 10; Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 365;
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                               0;
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                               Gaps
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APPLICANT: AGIATE, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6841
LENGTH: 373
TYPE: DNA
CODANIEM: HOMO SENSION
Search completed: November 16, 2002, 04:29:24 Job time: 49 secs
                                                                                       В
                                                                                                                                                                                                                                                                  US-09-867-701-6841
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                                                                                                                                                            Best Local Similarity 52.6%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapien
                                                                                     202 CCAATATAGTAAAACCACG 184
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                                                                                                                            1 CCAATNNNNNNNNNCCACG 19
                                                                                                                                                                   Score 10; DB 10; L
Pred. No. 4.4e+02;
Pred. No. 4.4e+02;
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